

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:09:25 ; Search time 24.8 Seconds
(without alignments)
1314.204 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292

Sequence: 1 MVEPQPTANSTRPMGAGPP.....FNIDPAPELRLPHLGIPTN 440

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SID88/gcgdata/geneseq/AA1980.DAT:*
2: /SID88/gcgdata/geneseq/AA1981.DAT:*
3: /SID88/gcgdata/geneseq/AA1982.DAT:*
4: /SID88/gcgdata/geneseq/AA1983.DAT:*
5: /SID88/gcgdata/geneseq/AA1984.DAT:*
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9: /SID88/gcgdata/geneseq/AA1988.DAT:*
10: /SID88/gcgdata/geneseq/AA1989.DAT:*
11: /SID88/gcgdata/geneseq/AA1990.DAT:*
12: /SID88/gcgdata/geneseq/AA1991.DAT:*
13: /SID88/gcgdata/geneseq/AA1992.DAT:*
14: /SID88/gcgdata/geneseq/AA1993.DAT:*
15: /SID88/gcgdata/geneseq/AA1994.DAT:*
16: /SID88/gcgdata/geneseq/AA1995.DAT:*
17: /SID88/gcgdata/geneseq/AA1996.DAT:*
18: /SID88/gcgdata/geneseq/AA1997.DAT:*
19: /SID88/gcgdata/geneseq/AA1998.DAT:*
20: /SID88/gcgdata/geneseq/AA1999.DAT:*
21: /SID88/gcgdata/geneseq/AA2000.DAT:*
22: /SID88/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1893.5	82.6	437	14	AA1980
2	561	24.5	477	22	AA1981
3	558.5	24.4	405	19	AA1982
4	557.5	24.3	400	14	AA1983
5	557.5	24.3	466	13	AA1984
6	554	24.2	405	15	AA1985
7	553.5	24.1	365	20	AA1986
8	552.5	24.1	400	15	AA1987
9	552.5	24.1	446	12	AA1988
10	552.5	24.1	446	14	AA1989
11	546	23.8	388	13	AA1990

12	533.5	23.3	487	18	AA1991	DI dopamine recept
13	531.5	23.2	446	12	AA1992	Rat dopamine DI re
14	531	23.2	402	11	AA1993	Beta 3 adrenergic
15	531	23.2	407	19	AA1994	Human adrenergic b
16	527.5	23.0	408	15	AA1995	Human beta-3 adren
17	527.5	23.0	487	12	AA1996	DI dopamine recept
18	508	22.2	379	18	AA1997	Corn barnacle G-pr
19	507.5	22.1	560	22	AA1998	Rat alpha-1a adren
20	507.5	22.0	565	22	AA1999	Human adrenocept
21	503	21.9	572	15	AA1990	Alpha 1a adrenerg
22	503	21.9	572	16	AA1991	Human alpha-1A adr
23	503	21.9	572	17	AA1992	Alpha-1A/D adrena
24	503	21.9	572	17	AA1993	Human alpha-1A adr
25	503	21.9	572	15	AA1994	Human alpha-1A adr
26	500	21.8	572	15	AA1995	Human alpha-1A adr
27	499.5	21.8	501	15	AA1996	Human alpha-1A adr
28	499.5	21.8	501	21	AA1997	Sequence of human
29	494.5	21.6	478	20	AA1998	Active form of hum
30	494.5	21.6	478	22	AA1999	Human serotonin re
31	493	21.5	515	22	AA1990	Hemster alpha-1b a
32	491.5	21.4	477	13	AA1991	Dopamine DI recept
33	491.5	21.4	501	16	AA1992	Human alpha-1A adr
34	489.5	21.4	572	15	AA1993	Sequence of human
35	488	21.3	477	16	AA1994	Dopamine receptor
36	488	21.3	477	18	AA1995	Human D5 dopamine
37	488	21.3	515	15	AA1996	Human/rat hybrid a
38	488	21.3	515	16	AA1997	Human/rat hybrid a
39	487.5	21.3	475	14	AA1998	Rat D1B dopamine r
40	486	21.2	515	21	AA1999	Mouse alpha-1b adr
41	485.5	21.2	501	22	AA1990	Human alpha-1aIpha
42	485.5	21.2	515	22	AA1991	Human adrenocept
43	484	21.1	515	22	AA1992	Rat alpha-1b adren
44	481.5	21.0	377	15	AA1993	G-protein coupled
45	481.5	21.0	377	17	AA1994	G-protein coupled

ALIGNMENTS

RESULT 1
ID AAR36801 standard; Protein: 437 AA.
AC AAR36801;
XX
XX
25-AUG-1993 (first entry)
XX
XX
Rat serotonin St-B17 receptor.
XX
XX
DE
XX
XX
Polymerase chain reaction; primer: PCR; amplify: rat; serotonin;
XX
XX
G-protein; receptor: catecholamine; St-B172; St-B17; drug: CNS;
XX
XX
Intron; splice: clone: transmembrane; 5-HT; family: hydrophobic;
XX
XX
5-HT2; 5-HT1D; 5-HT1C; 5-HT1B; 5-HT1A; 5-HT1E.
OS
XX
XX
Synthetic.
XX
XX
US7970338-A.
XX
XX
01-APR-1993.
XX
XX
26-OCT-1992; 92US-0970338.
XX
XX
26-OCT-1992; 92US-0970338.
XX
XX
(USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
XX
Monsma FJ, Sibley DR;
XX
XX
WPI: 1993-159491/19.
XX
XX
N-PSDB; AA041701-2.
XX
XX
Cloned gene encoding serotonin St-B17 receptor gene - used to
XX
XX
test drugs for CNS activity

XX Disclosure; Page 31-33; 51pp; English

This sequence encodes the rat serotonin St-B173 receptor and was encoded by the clone St-B173. The putative intron, found in clone St-B172, was absent from this clone with the flanking exons being spliced together at nucleotide 873. Splicing at this position results in a 1311 bp open reading frame encoding a protein of 437 amino acids with a molecular weight of 46.8 kD. Hydrophobicity analysis of this amino acid sequence indicated several hydrophobic regions predicted to represent putative transmembrane spanning domains. When compared to previously cloned G-protein coupled receptors, the transmembrane regions of St-B17 exhibited high homology to various serotonin (5-HT) receptors suggesting that it may be a member of this receptor family. Within the transmembrane regions, St-B173 exhibits homology of 41%, 38%, 38%, 37% and 36% with 5-HT₁, 5-HT₂, 5-HT₃, 5-HT₄, 5-HT₅ and 5-HT₆ receptors respectively. The isolated gene, St-B17, encodes a protein which may be used to test CNS activity of drug candidates.

Sequence 437 AA;

Query Match	82.6%;	Score 1893.5;	DB 14;	Length 437;
Best Local Similarity	84.3%;	Pred. No. 8.2e-176;		
Matches 375;	Conservative 11;	Mismatches 46;	Indels 13;	Gaps 4;

[illegible]

RESULT 2

ID AAB70765 standard; Protein; 477 AA

AC AAB70765

DT 18-MAY-2001 (first entry)

Human beta1-adrenoreceptor protein.

KW **Beta1-adrenoreceptor; human; mutation; disease predisposition;**

XX

OS	Homo sapiens.
XX	
PN	WO200111039-A2.
XY	

This invention describes a novel human beta1-adrenoreceptor gene (I) that comprises 1-7 or more mutations, excluding the sequence with the mutations Ala145Gly or Gly116Ser. The invention also describes (1) a method for determining predisposition to disease by genotyping DNA of (1) at one or more exchanged position and comparison with a reference sequence; and (2) a new variant of the beta1-adrenoreceptor (II) which include at least one of the amino acid changes Ser49Gly, Ala55Ser, Gly3389Arg, Arg3399Gly, His402Arg, Thr404Ala and/or Pro418Ala, but excluding the sequence with a single amino acid exchange at positions 49 or 389. Genotyping of (I) is used to determine predisposition to cardiomyopathy, specifically the dilative form, also for prognosis and assessing severity of this condition. Gene (I) can be used for the following: (i) development of therapeutic agents, especially a new class of beta1-adrenoreceptor (ant)agonists; (ii) construction of genes or vectors, especially for pharmaceutical development; and (iii) develop diagnostic kits, particularly for determining predisposition and individual responses to different beta1-adrenoreceptor (ant)agonists, including predisposition to develop side effects and habituation.

Sequence 477 AA;

Query Match	24.5%;	Score 561;	DB 22;	Length 477;
Best Local Similarity	34.3%;	Pred. No. 4.6e-46;		
Matches 148;	Conservative 66;	Mismatches 161;	Indels 56;	Gaps 14;

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OY      1  MPEBGPSTANSTPMWAGAPBPAPGSGVAAALCVVIALTPMAANSLITALICTOPALRNT 60
Db      33  lvpasppslilppasegepreltsqwtsgmglmlmlvlvlvgaqvrvlvalaktprql 92
OY      61  SNFVLVSFTSDLWAGLVYMPAPMILNALYKRWYIARGLCLMTRFVDMCCSASILNLCI 120
Db      93  tnlflmsiasadlmgjllvlpfgaltlvwvgwsgsfccelwetsvdvlcvlasletclvl 152
OY      121  SUDRVLILSPRLRYKLRMTPLRALVALYLGANSLAALSPFLLELGM--HELGHARPPV-- 176
Db      153  aldryaltspfrigslltrrarqylctvaiaiaysfipilmhwwraesdearrcynd 212
OY      177  PGQCRILASLPFVLVAGSLFFLPDSGAICFTYTHILLARKQAVQVS----LTTGMAQO 232
Db      213  pkccdfvtnrayaiaassvsfylvdlcmafyllvfreaqgyvkkidscerrllgpparp 272
OY      233  ASET-----LQYPRPRPGEVSADS-----RLRAIKSRKALAKLVITGITL 273
Db      273  pspspsvpbadpppgpprppaaataaplanguagkrtrpslvalteqalk---tlgil 329
OY      274  LGMFEVTLMPFVANIYQAV--CDCISPLQLEPDLVTMLQCYCSTNMNPITY---PLFMRDFKR 329
Db      330  mgvflwclpffliianvkafrnelvpdrllfvfnwlgysanafrpilycrrsp-----dfik 385
OY      330  ALGRRLPCPR---CPREKQASLASPLSLRTSHSGRRGLS---LQOVLPLPLP--PDSQSDSD 383

```

DB 386 atfgrllccaracrr-----raah-gdiprasgclaraqpppsgaasddddd 433
 QY 384 AGSGSGSSGLRL 394
 DB 434 dvvgatpparl 444

RESULT 3

AAW44933
 ID AAW44933 standard; Protein: 405 AA.

AC AAW44933;

DT 14-OCT-1998 (first entry)

DE Canine beta-3 adrenergic receptor.

KW Canine; beta-adrenergic receptor; brown adipose tissue; probe: human;
 hybridisation; ligand; ss.

XX Canis familiaris.

EH Key Location/Qualifiers

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated"

FT Domain /label= "transmembrane domain 1"

FT Domain /label= "transmembrane domain 2"

FT Domain /label= "transmembrane domain 3"

FT Domain /label= "transmembrane domain 4"

FT Domain /label= "transmembrane domain 5"

FT Domain /label= "transmembrane domain 6"

FT Domain /label= "transmembrane domain 7"

PN W09735973-A2.

PD 02-OCT-1997.

XX 26-MAR-1997; 97WO-FR00537.

XX 26-MAR-1996; 96FR-0003730.

XX (VERT-) VETIGEN.

XX Drumare MF, Lenzen G, Pietri-Rouxel F, Strosberg AD;

DR WPI: 1998-032136/03.

XX N-PSDB: AAV30469.

PT Canine beta 2 and beta 3 adrenergic receptors and coding sequences -
 useful for identifying specific ligands and (ant)agonists to develop
 specific treatments for obesity in dogs

PS Claim 3; Page 54-55; 79pp; French.

XX This sequence represent the canine beta 3-adrenergic receptor

CC (RA-Ca-b3). The coding sequence was isolated from a cDNA library

CC constructed from polyA+ RNA purified from dog brown adipose tissue cells.

CC The probe was a fragment of the coding region of the human beta-3

CC adrenergic receptor covering the region from the initiation codon to

CC transmembrane domain 7 (TM7) amplified by primers AAV30511-V30512. The

CC full length insert was cloned into M13 for sequencing using primers

CC AAV30470-V30490. The sequence can then be expressed e.g. in a mammalian

CC cell, by subcloning into an expression vector such as pCDNA3. RA-Ca-b3

CC has been implicated in obesity and obesity-related metabolic disorders

CC e.g. diabetes. The canine version of RA-Ca-b3 can be used to develop
 CC treatments specific for dogs. The sequence can also be used in the beta-2
 CC differential screening for ligands for RA-Ca-b3 as compared to the beta-2
 CC adrenergic receptor (AAW44932).

SQ Sequence 405 AA;

Query Match 24.4%; Score 558.5; DB 19; Length 405;
 Best Local Similarity 35.6%; Pred. No. 6.5e-46;
 Matches 148; Conservative 59; Mismatches 154; Indels 55; Gaps 15;

QY 3 PECPPTANTPAMAGPPSPAGSGGWAALCVIALTAANSILIALCTCPALRNTSN 62
 DB 18 pcpptant-----s9lpapwavalagallalevalatvgnlivlvalartprlqumcn 73
 QY 63 PFLVSLFTSDLVWGLVMPVPMALNLYGHWVLARGCLMTAFDWCSSASILNCLISL 122
 DB 74 vftstlatdvlvgllvvpqatlaltgtrwpgatgcwtsvdvlcvstasietlcalav 133
 QY 123 DRYLLILSPLRKRLRMTPLRALALVGAWSLAALASFLPLLGWHELG-----HARP 174
 DB 134 drylavtnplrygalvtkraraavlvwvsaavsfapimskwrvgaadaeqchsnp 193
 QY 175 PVPGCCRLASLPVLVAGSLPFLPSGALCFPTCYHLLAARKQAVQVASTLTGMASQAS 234
 DB 194 hc-----cafasnlpvalissvsfypdlvmlfyaavtlvatcrg-lrlllrrelgrfppe 249
 QY 235 ETLQVPRPRPG-----VESADSR--RLATKHSRKALAKLTLLGLGMFEVWL 282
 DB 250 sppaasrstrppparrrcaapaavpdrllrparllprhrrair---lglvgftfclwl 306
 QY 283 PRFVANIVQAVCD---CISPGLEFVLTWLGYNSTNPIITY---PLFMRDKRALGRFP 336
 DB 307 pftvanvmtalgpslvspall-almwlgynasfnpllycrsp---dftsatfrll- 360
 QY 337 CPRCPREQASLASPSLRTSHSGPRGLSLQGVLPPLPPDSUSDSDACSGSSGL 392
 DB 361 c-rrtrehrraasp-----pqdpsaapaaltspaes-stcgaiddgsygl 404

RESULT 4

AAAR2501
 ID AAR2501 standard; Protein: 400 AA.

AC AAR2501;

DT 09-JUN-1993 (first entry)

DE Beta-adrenergic receptor.

XX Fat cell specific; BAR; lipolysis; obesity; diagnosis;

KW thermogenesis; metabolism.

XX Rattus rattus.

PN US7783602-A.

PD 15-DEC-1992.

PF 11-NOV-1991; 91US-0783602.

PR 01-NOV-1991; 91US-0783602.

XX (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI Venter CJ;

DR WPI: 1993-067426/08.

XX Fat cell specific beta- adrenergic receptor polypeptide - used
 PT for diagnosis of obesity due to inactive lipolysis

XX


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FT FT /note= "transmembrane region 1 (TM1); see AAR70668"
FT FT 76..99
FT FT /note= "transmembrane region 2 (TM2); see AAR70669"
FT FT 110..131
FT FT /note= "transmembrane region 3 (TM3); see AAR70670"
FT FT 156..178
FT FT /note= "transmembrane region 4 (TM4); see AAR70671"
FT FT 203..26
FT FT /note= "transmembrane region 5 (TM5); see AAR70672"
FT FT 293..314
FT FT /note= "transmembrane region 6 (TM6); see AAR70673"
FT FT 322..347
FT FT /note= "transmembrane region 7 (TM1); see AAR70674"
XX XX
XX XX W09424162-A.
XX XX 27-OCT-1994.
XX XX 21-APR-1994; 94WO-FR00447.
XX XX 21-APR-1993; 93FR-0004670.
XX XX 21-APR-1993; 93FR-0004670.
XX XX (VETI-) VETIGEN.
XX XX (VETI-) VETIGEN.
XX XX Kapoor A, Lenzen G;
XX XX WPI; 1994-341770/42.
XX XX N-PSDB; AAO74367.
XX XX
XX XX New nucleic acid encoding the bovine beta3 adrenergic receptor -
XX XX are related peptide(s), vectors and transformed cells, useful for
XX XX identifying specific agonists and antagonists
XX XX
XX XX Claim 16; Page 3-5; 52pp; French.
XX XX
XX XX AAR62515 shows the amino acid sequence of the bovine beta3 adrenergic
XX XX receptor encoded by AAO74367. The peptide contains 7 transmembrane
XX XX regions, all of which are claimed individually and are useful for the
XX XX generation of probes for screening compounds that have
XX XX agonist/antagonist activity to the receptor. (See AAR70668-74). These
XX XX probes are specific to the beta3 gene and not to beta1 or beta2 genes.
XX XX These cpts. could be used to regulate the level of fat in animals,
XX XX partic. for improved meat quality.
XX XX
XX XX Sequence 405 AA:
SQ

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Query Match 24.2%; Score 554; DB 15; Length 405;
Best Local Similarity 33.6%; Pred. No. 1.8e-45;
Matches 143; Conservative 61; Mismatches 156; Indels 66; Gaps 13;

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OY 1 MWPEPG-PTANSTPMAGAPPSAGSGVAAALCVIALTAANSLLIALICTOPALRN 59
DB 11 ltpwfdlptlanptanaglpqvpwavalagallavlatvgngllvalatartpigt 70
OY 60 TSNFVLVSFTSDLMVGLVMPAMLNALYGRWVLARGICLMTAFDVMCCSASILNCL 119
DB 71 mtnvfvrtlatdvlvgllvppgaclaltgmplvgvscelvtadvdlcvlastletcla 130
OY 120 ISLDVYLLISPLRYKRLMTPLRALALVIGAWSLAASFLPDLGLGWHELG-----H 171
DB 131 lavdtylavtmpltygalvltkrralaavlyvvvsaavsfapimskwrtigadaeaqrch 190
OY 172 ARPVPGOCRLASLPFVLVAGSLTFPLPSAICTYCRILLAARKQAVOVASLTFTGM-- 229
DB 191 snprc---ctfasmpmyallsssvsfypllmvltyvarfvatrrq-lrllrrelgrfp 246
OY 230 -----ASQASERLOVPRTRPRGVESADSR--RLATKHSKALKAKILTLGLGMFV 279
DB 247 peespaprsrsgplagpcasagvpsyrparllplrehrafr---tlgllngftfl 303
OY 280 TWLPFFVANIVAV--CDCISPGLEFDVLTWLGYSNSTMNPILY---PLFMRDFKRALGRF 334

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DB 304 cwlpifvvnvtaigpslvsptflalnwiqyansafiplyicrpsdfrllctc 363
OY 335 LP-----CPRCPREORASLASPLRSHSGPRPGSLAQVLPLPDPDSDSADGS 386
DB 364 rpeehlaaasppraps-----gapaltspagpnmq-----ppeld----- 398
OY 387 GGSSGL 392
DB 399 gascgl 404

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RESULT 7
AA13737
ID AA13737 standard; Protein; 365 AA.
XX AC AA13737;
XX AC
XX DT 13-SEP-1999 (first entry)
XX DE
XX DE Murine beta-1 adreno-receptor.
XX XX Human; amine receptor; recombinant; murine; beta-1 adreno-receptor.
XX XX Mus sp.
XX OS
XX PN US5928890-A.
XX PN
XX PD 27-JUL-1999.
XX PF 06-JUN-1995; 95US-0467559.
XX PR 06-JUN-1995; 95US-0467559.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Li Y;
XX DR WPI; 1999-429497/36.
XX XX
XX XX Human amine receptor polynucleotides, vectors and host cells
XX XX
XX XX Disclosure; Fig 2; 22pp; English.
XX XX
XX XX The invention relates to a human amine receptor polypeptide. Host cells
XX XX transformed with a vector comprising the amine receptor coding sequence
XX XX are used for the recombinant production of the polypeptide. The
XX XX polypeptides are useful for treating conditions related to under-
XX XX expression and over-expression of the human amine receptor. The present
XX XX sequence represents a murine beta-1 adreno-receptor.
XX XX
XX XX Sequence 365 AA:
SQ

Query Match 24.1%; Score 553.5; DB 20; Length 365;
Best Local Similarity 37.8%; Pred. No. 1.7e-45;
Matches 137; Conservative 56; Mismatches 134; Indels 35; Gaps 12;

```

OY 7 PTANSTPMAGAPPSAGSGVAA--ALCVIALTAANSLLIALICTOPALRNTSNF 63
DB 9 ppsallppaseg--saplsqvtlagmgllvalivllvvgngllvalalakprjqlclnl 66
OY 64 FLVSLFTSDLMVGLVMPAMLNALYGRWVLARGICLMTAFDVMCCSASILNCLISLD 123
DB 67 flmslasadlvngllvvpfgatlvwgrwvgsffcelwtsvdvlcvlastletclavald 126
OY 124 RVLTLSPRLRYKRLMTPLRALALVIGAWSLAASFLPDLGLGW-----HGHARPV--PQ 179
DB 127 tyaltsprryslltrataivctwaaisalvflpllmhwtreesdeatregndpc 186
OY 180 CRLASLPFVLVAGSLTFPLPSAICTYCRILLAARKQAVOVAS--LFTGMASQAS- 234
DB 187 cdfvncrnyalasvsvsfyvpclmafylylrfrdaqgvkklidccerrflgpparppsp 246

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```

0Y      235 EFLQVPRPFGVESADSR-----RLATKHSRKALKAKLTGLTGLGFEFTWLPDEFVA 287
Db      247 epspspgppripdadsiangrskrrperivalregalk---tlgimgyftlcwlpflia 303.
0Y      288 NIVQAV-CDICISPGLEFDVLTWLGYCNSIWNPIITY--PLFMRDPFKALGRFLPCPR--C 340
Db      304 nvvkaefhdldvpdrifvfwnwlgynasafnpllycrsp----dfrikafgllccarraac 359
0Y      341 PR 342
Db      360 rr 361

RESULT      8
AAR54992
ID      AAR54992 standard; Protein; 400 AA.
XX
XX      AAR54992;
XX
XX      23-JAN-1995 (first entry)
DE      Murine beta-3 adrenergic receptor.
XX
XX      Receptor; beta; adrenergic; testing; screening; identification;
KW      drugs; adenylate cyclase; hormone; lipase; signal transduction.
XX
XX      Mus musculus.
PN      EP600136-A.
XX
XX      08-JUN-1994.
XX
XX      01-DEC-1992;    92EP-0403248.
XX
XX      PR      01-DEC-1992;    92EP-0403248.
XX
XX      (CNRS ) CENT NAT RECH SCI.
PA      Emorine L, Nahmias-kaminski C, Strosberg AD;
XX
XX      WPI: 1994-177542/22.
DR      N-PSDB; AAO65477.
XX
XX      Isolated and purified polypeptides having beta3-adrenergic
PT      receptor activity - are used to study the effects of various
PT      chemical agents on the beta3-adrenergic receptor
XX
XX      Claim 2; Figure 4; 15pp; English.
XX
XX      The coding sequence of the beta-three adrenergic receptor can be
CC      used in expression vectors which are then used to transform cells.
CC      The cells then express the receptor on their surfaces and can be
CC      used to study the effects of various chemical agents on the receptor
XX      which is coupled to adenylate cyclase and hormone sensitive lipases.
XX
XX      Sequence      400 AA;

Query Match          24.1%; Score 552.5; DB 15; Length 400;
Best Local Similarity 35.1%; Pred. No. 2.4e-45;
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15

0Y      5 PGPRTNSTPPA-GGACP---PSAPGGSG-----WVAALCVIAL-TAAANSLLIALICYQ 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3 pwpfhngslalsadapldpsaaatsqldpywaalagallatalatvggnllvialart 62

0Y      55 PALRMTSNEFIYSLEFTSDLMVGLVYWPPAMLNALYGRWYLARGCLDLMTAFDVMCCASAI 114
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      63 plgtlctntfvsclsaadalvlgllvmppactalclghwplglgetcelvsvdalcvtlaai 122

0Y      115 LNLCLISLDRIYLLISPLRYKLMPPLRALALVLCAMSLAASFLPLLIGMHELG---- 170
| | : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY	171	----	HARPVVGQGRCLASLPFLVVAAGLTFPLPSGAICTCYICLILAAKQAVQVNASLT	226
Db	123	etlcalavdrylawnlpjryglvtckrrraaavlwivsaavsfpapimsqmwivgdae	162	
QY	171	---- <th>HARPVVGQGRCLASLPFLVVAAGLTFPLPSGAICTCYICLILAAKQAVQVNASLT</th> <th>226</th>	HARPVVGQGRCLASLPFLVVAAGLTFPLPSGAICTCYICLILAAKQAVQVNASLT	226
Db	183	aqechsnprc---csfasimpyallsssvstlylpilvmltyavivvakrrqr-hllrr	238	
QY	227	TGMAQSASETLQVRETRP-----	GVESADSR--RLATYHSRKALKAKLTGLL	274
Db	239	lgrtspespspspspspspspatgftgaapdgyppcgrrrrpallprrhrarrr---tlglim	295	
QY	275	GMEFVTMLPFVANIIVAVC--DCISGLDELVTWLCYCNSTMPPIY---	PLFMRDFKR	329
Db	296	gfislcwlpffllaviralagpslvpqsvfialnmlyghansafnpvlycrspofrdafr	355	
QY	330	AL----	GRFLPCPRC---PREQASLASPSLR--TSSGGRP	362
Db	356	llcsygrgrgpeeprravtcfpsvpaarspplnrtidgyegarp	397	
RESULT	9			1
AAR15498	ID	AAR15498	standard; Protein; 446 AA.	
XX	AAR15498;			
XX	08-MAR-1992	(first entry)		
XX	Human dopamine D1 receptor.			
DE				
XX	catecholamine; G-protein-coupled receptor; neurotransmitter;			
KW	adenylyl cyclase stimulation.			
XX	Homo sapiens.			
OS				
XX	Key	Location/Qualifiers		
FT	Modified-site	5		
FT		/label= OTHER		
FT		/note= "N-glycosylation site - putative"		
FT	Modified-site	175		
FT		/label= OTHER		
FT		/note= "N-glycosylation site - putative"		
FT	Domain	23..49		
FT		/label= transmembrane		
FT		/note= "I"		
FT	Domain	62..87		
FT		/label= transmembrane		
FT		/note= "II"		
FT	Domain	94..120		
FT		/label= transmembrane		
FT		/note= "III"		
FT	Domain	138..164		
FT		/label= transmembrane		
FT		/note= "IV"		
FT	Domain	192..218		
FT		/label= transmembrane		
FT		/note= "V"		
FT	Domain	273..299		
FT		/label= transmembrane		
FT	Domain	311..337		
FT		/label= transmembrane		
FT		/note= "VI"		
FT	Region	265..268		
FT		/label= Protein_kinase_A_phosphorylation_site		
FT		/note= "putative"		
FT	Region	338..343		
FT		/label= Protein_kinase_A_phosphorylation_site		
FT		/note= "putative"		
XX	W09118005-A.			
XX	28-NOV-1991.			
XX				
XX				

Db 300 sgetcpicidnsntdvtwfgwanslnpiiy-afnadfrkafstllgcyfcpatnna 358
OY 347 -----SLASPELPTSHSGRPGLSLQVLPPLPDDSDSDAGSGSSGLRLTAQLLP 401
Db 359 etvinnngaaamfshhepysiskcnlyllphnavyssedlkkeeaaiarplekisp 418
OY 402 GEATQDPPPLPRAAAAVNFENIDPAEPELRP-----HP 434
Db 419 -----alsvldydtvstlektpitqngqhp 445

RESULT 11
AAR25698 standard; Protein: 388 AA.
XX AAR25698;
XX AAR25698;
XX 20-JAN-1993 (first entry)
XX Murine adrenergic beta-3 receptor.
XX Mouse; polymerase chain reaction; transmembrane region;
XX adrenergic receptor.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 36..60 /label= transmembrane
FT /label= transmembrane
FT 70..97 /label= transmembrane
FT Domain 110..129 /label= transmembrane
FT Domain 153..175 /label= transmembrane
FT Domain 201..222 /label= transmembrane
FT Domain 290..311 /label= transmembrane
FT Domain 324..344 /label= transmembrane
FT Domain /label= transmembrane

XX W09212246-A.
XX 23-JUL-1992.
XX 14-JAN-1992; 92MO-FR00023.
XX 14-JAN-1991; 91FR-0000320.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Emorine LJ, Nahmias C, Strosberg AD;
XX WPI; 1992-268668/32.
XX N-PSDB; AAO26808.
XX Murine adrenergic beta-3-receptor and nucleic acid encoding it -
XX for treating diabetes, obesity and hyperlipidaemia, and also for
XX identifying ligands with beta-3 affinity
XX
XX Claim 13; Page 37; 61pp; French.
XX The murine beta-3 adrenergic receptor gene encodes a polypeptide
XX with 82% homology with the human beta-3 adrenergic receptor. The
XX homology is concentrated in the 7 transmembrane domains.
XX See also AAO26804-7.
XX Sequence 388 AA;
XX

Query Match 23.88; Score 546; DB 13; Length 388;

Best Local Similarity 35.98; Pred. No. 1e-44;
Matches 139; Conservative 59; Mismatches 137; Indels 52; Gaps 16;
OY 5 PCPTANSTPA-WGAGP---PSAPGSG-----WVAALCVIAL-TAANSILALICIQ 54
Db 3 pwrhngslalswadapcltdpsaantsglpyvwaalagalalatalvgallvialart 62
OY 55 PALRNTSNFELVSLFTSDLMGLVMPAMLNALYGRWVLARGCLLMTAFDVMCCSASI 114
Db 63 prlgticnvftvstlaadlvlgllvmppgalaltgmipgetgcetvcelvsvdvicvst 122
OY 115 LNLCLISLDRYLLILSLPRKRLKMTPLRALALVIGANSLSAASFLLGLGHELG---- 170
Db 123 etlcalavdrylavtnplrygtclvtkraraavylvlsaaavsfapimgvrvgadae 182
OY 171 ---HARPPVGGCRLLASLDFVLVAGLPELFGAICFYCRILLAAKQAOVAVSLT 226
Db 183 aqechsnprc---csfsamvyalissvstfpllmvltvavrfvavrqr-hllrre 238
OY 227 TGMASQASSETLQVPRTRP-----GVESADSR--RLATRHSKALKAKLTGL 274
Db 239 lgrfspeesppsparspspatgftpaapdyppcgrrparllplrehalr---tlglim 295
OY 275 GMFVTVLPFFVANIVQAVC--DCISPEGLFDVLTWLGCONSTNMPITY---PLFMRDFKR 329
Db 296 gflslcwlplflaviralagpslvpsgvfialawlgysafnpylvcvscp---dfird 351
OY 330 ALGRFLPCP---RCPREROASL--ASP 351
Db 352 aftrll-csyg9g9gpepravtfrpsp 377

RESULT 12
AAM09795 standard; Protein: 487 AA.
XX AAM09795
XX AAM09795;
XX 11-JUN-1997 (first entry)
XX
XX Key Location/Qualifiers
FH 45 /note= "N-linked glycosylation site"
FT Modified-site
XX
XX US5610282-A.
XX 11-MAR-1997.
XX 06-JUL-1990; 90US-0548714.
XX 06-JUL-1990; 90US-0548714.
XX 06-JUL-1990; 90US-0548714.
XX 11-MAR-1993; 93US-0023917.
XX 19-MAY-1995; 95US-0444734.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Mahan LC, Mcvittie LD, Monsma FJ, Sibley DR;
XX WPI; 1997-178452/16.
XX N-PSDB; AAT63657.
XX DNA encoding D1 dopamine receptor protein - for production of
XX transformed cells used for drug screening
XX
XX Claim 1; Column 11-16; 24pp; English.

XX The sequence is the rat D1 dopamine receptor protein which is linked to
 CC the activation of adenylyl cyclase activity. The receptor also couples
 CC with guanine nucleotide binding regulatory (G) proteins. By constructing
 CC cell lines that express the D1 receptor, the affinities and efficacies of
 CC agonist and antagonist drugs can be assessed.

XX Sequence 487 AA;

Query Match 23.3%; Score 533.5; DB 18; Length 487;
 Best Local Similarity 33.3%; Pred. No. 2.2e-43;
 Matches 134; Conservative 72; Mismatches 157; Indels 39; Gaps 12;

OY 30 AALCVIALTAANSLLIALICTOPALRN-TSNFELVLSFTSDLMVGLVYMPAMNLAL 88
 Db 67 acfislillstlgnltvcaaviftrhlrskvtnftvislavsdllyavlympkavael 126
 OY 89 YGRWVLAAGLCILMTAPDVMCCSASTLNLCLISDRYLLISPLRYKLRMTPLRALAVL 148
 Db 127 agfwpfpg-pfcniwafidmstaslnlcvlsvdrwaispfigyerkmpkaafllis 185
 OY 149 GAWSLAALASEFLPLLGMHELGHARP--PVPG-----OCRLASLPFVLVASGL 195
 Db 186 vawtlsvlslfipyqlswkh---akptwpldgntfsltdeddnodtrlsrtyaisssli 242
 OY 196 TEFPLPSGALICTYCRILLAARKQAVQVAST--TTGMAASGASFTLQVPRPRGVSADSR 254
 Db 243 stfypvalmivtyslrylaqgqtrrsaleraavhancqtltagngnrvccasgessfk 302
 OY 255 LATKSRKALAKLTGLIGLMEFTWMLPFVAVNTQAVCD-----CISPGLEFDVLTW 307
 Db 303 msfkrctkvk---tlavimgvfvcwlpfflscnmpfcgseeqpciclsitfdvfw 359
 OY 308 LGYCNSTWNPITTYPLFMDERKALGRFLPCPR-CPRERQASIASPSLR-----TSHSG 359
 Db 360 fgwanssimpliy-afnfdqkafstllgyrlcptlna-ietvsinnngavvsshe 417
 OY 360 PRPGSLDQVLPPLPPSDSDSAGSGSGRLRTAOLLPL 401
 Db 418 prgsiskdcnlvyliphavgsedlkkkeagglakpleklsp 459

RESULT 13

AAR15499
 ID AAR15499 standard; Protein; 446 AA.

XX AAR15499;

08-MAR-1992 (first entry)

Rat dopamine D1 receptor.

KW catecholamine; G-protein-coupled receptor; neurotransmitter;
 KW adenylyl cyclase stimulation.

XX Rattus rattus.

XX Location/Qualifiers

FT Key 4
 FT Modified-site /label= OTHER
 FT Modified-site /note= "N-glycosylation site - putative"

FT Modified-site 174
 FT Modified-site /label= OTHER

FT Modified-site 135
 FT Modified-site /note= "N-glycosylation site - putative"

FT Modified-site 229
 FT Modified-site /label= Protein_kinase_A_phosphorylation_site

FT Modified-site 268
 FT Modified-site /note= "putative"

FT Modified-site 268
 FT Modified-site /label= Protein_kinase_A_phosphorylation_site

FT Modified-site 268
 FT Modified-site /label= Protein_kinase_A_phosphorylation_site

FT /note= "putative"

XX M09118005-A.

XX 28-NOV-1991.

XX 13-MAY-1991; 91WO-US03308.

XX 17-SEP-1990; 90US-0583852.

XX 14-MAY-1990; 90US-0523237.

XX (UYDU-) DUKE UNIV.

XX (UYOR-) OREGON HEALTH SCI UNIV.

XX Bunzow JR, Civelli O, Grandy DK, Zhou OY, Caron MG;
 PI Deary A, Falardeau P, Gingrich JA;

DR WPI: 1991-369177/50.

DR N-PSDB: AAQ14955.

PT Cloned gene encoding D1-dopamine receptor - useful for e.g. drug
 PT screening, diagnosis of e.g. Parkinson's disease or schizophrenia
 PT or in gene therapy

PS Example 9; Fig 3A; 52pp; English.

CC The D1 dopamine receptor sequence was obtained from two overlapping
 CC clones, one genomic and the other from a rat striatum cDNA

CC library. The amino acid sequence was deduced from the

CC nucleotide coding sequence. The receptor is similar to the human D1

CC dopamine receptor (see AAR15498) and known G-protein coupled proteins,

CC e.g. Cys(351) in the carboxyl terminus is conserved in most G-protein

CC coupled receptors; it may be palmitoylated. The carboxyl tail also

CC contains several putative sites for phosphorylation by an agonist-

CC dependent receptor kinase.

XX Sequence 446 AA;

Query Match 23.2%; Score 531.5; DB 12; Length 446;
 Best Local Similarity 33.1%; Pred. No. 3.1e-43;
 Matches 133; Conservative 72; Mismatches 158; Indels 39; Gaps 12;

OY 30 AALCVIALTAANSLLIALICTOPALRN-TSNFELVLSFTSDLMVGLVYMPAMNLAL 88
 Db 26 acfislillstlgnltvcaaviftrhlrskvtnftvislavsdllyavlympkavael 85
 OY 89 YGRWVLAAGLCILMTAPDVMCCSASTLNLCLISDRYLLISPLRYKLRMTPLRALAVL 148
 Db 86 agfwpfpg-pfcniwafidmstaslnlcvlsvdrwaispfigyerkmpkaafllis 144
 OY 149 GAWSLAALASEFLPLLGMHELGHARP--PVPG-----OCRLASLPFVLVASGL 195
 Db 145 vawtlsvlslfipyqlswkh---akptwpldgntfsltdeddnodtrlsrtyaisssli 201
 OY 196 TEFPLPSGALICTYCRILLAARKQAVQVAST--TTGMAASGASFTLQVPRPRGVSADSR 254
 Db 202 stfypvalmivtyslrylaqgqtrrsaleraavhancqtltagngnrvccasgessfk 261
 OY 255 LATKSRKALAKLTGLIGLMEFTWMLPFVAVNTQAVCD-----CISPGLEFDVLTW 307
 Db 262 msfkrctkvk---tlavimgvfvcwlpfflscnmpfcgseeqpciclsitfdvfw 318
 OY 308 LGYCNSTWNPITTYPLFMDERKALGRFLPCPR-CPRERQASIASPSLR-----TSHSG 359
 Db 319 fgwanssimpliy-afnfdqkafstllgyrlcptlna-ietvsinnngavvsshe 376
 OY 360 PRPGSLDQVLPPLPPSDSDSAGSGSGRLRTAOLLPL 401
 Db 377 prgsiskdcnlvyliphavgsedlkkkeagglakpleklsp 418

RESULT 14


```
Db      70 mhnvfvtslaaadlvmgllvypaactlaltghmpigatgcclwtsvdvlcvrasietlca 129
Oy      120 ISLDRTLLILSPRLKLNMTPLRLALALVIGANSLAALASFPLLLGWHELG-----H 171
Db      130 lavdiylavtnplrygalvtkrcartavvlwvvsaaavsfapimsgwtrvgadaeaqrch 189
Oy      172 ARPPVGGCRLIASLPFVIVASGLTFEPLPSGAICTYCRILLARKQAVQVASTTGMAS 231
Db      190 snprc---cafasmppvylsssvsfylpdlvmlfyarvtrvalcrq---lrlrgelg 242
Oy      232 Q--ASETLQVPR-----TPRPGVESADSR--RLATKHSRKALKAKLTGLGILGM 276
Db      243 rfppeesppaprsiapapvytcappegypacgrrparllplrehral---ctlgimgt 299
Oy      277 FFVWTWLPFFVANIVQAV-CDCTSPG-LFDVLTWLGVCNSTMNPITY---PLFMRDFKRAL 331
Db      300 flcwlplfflanvrlalggpslvpgpafialnwlgyansafnpllycrspdfrsafrll 359
Oy      332 ---GRFLPCPCPCRREROASLAS--PSLRTSHSGPR 361
Db      360 crcgrrlppepcaarpalfpsgvpaaarsspaqr 394
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Search completed: March 15, 2002, 14:11:21
Job time: 116 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:10:55 ; Search time 13.3 Seconds
(without alignments)
1212.972 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292
Sequence: 1 MVPEPPTANSTPMAGAPP.....FNIDPAPPELPHPLGIPTN 440

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	2287	99.8	440	1	5H6_HUMAN
2	1989	86.8	440	1	5H6_MOUSE
3	1678	73.2	436	1	5H6_RAT
4	591.5	25.8	466	1	BIAR_MOUSE
5	587.5	25.6	473	1	BIAR_CANFA
6	586.5	25.6	466	1	BIAR_RAT
7	571	24.9	474	1	BIAR_FELCA
8	563.5	24.6	480	1	BIAR_MACMU
9	559	24.4	468	1	BIAR_PIG
10	558.5	24.4	405	1	BIAR_CANFA
11	557.5	24.3	467	1	BIAR_BOVIN
12	557	24.3	477	1	BIAR_HUMAN
13	554	24.2	405	1	BIAR_BOVIN
14	553.5	24.1	405	1	BIAR_SHEEP
15	552.5	24.1	400	1	BIAR_MOUSE
16	552.5	24.1	446	1	DADR_HUMAN
17	552.5	24.1	467	1	BIAR_SHEEP
18	551.5	24.1	400	1	BIAR_RAT
19	550.5	24.0	405	1	BIAR_CAPHI
20	548.5	23.9	466	1	DADR_MACMU
21	547.5	23.9	363	1	DADR_CARAU
22	543.5	23.7	418	1	BIAR_MACMU
23	539.5	23.5	398	1	BIAR_FELCA
24	538.5	23.5	446	1	DADR_PIG
25	538	23.5	386	1	DADR_OREMO
26	535.5	23.4	428	1	B4AR_MEIGA
27	533.5	23.3	446	1	DADR_RAT
28	531	23.2	408	1	BIAR_HUMAN
29	530.5	23.1	446	1	DADR_DIDMA
30	528.5	23.1	463	1	D5DR_PUGRU
31	526.5	23.0	483	1	BIAR_MEIGA
32	524.5	22.9	459	1	D1DR_FUGRU
33	524	22.9	351	1	B3AR_CAVPO

34	516	22.5	511	1	D0PL_DROME	P41596 drosophila
35	512.5	22.4	576	1	AIAD_RABIT	O02666 oryctolagus
36	508	22.2	379	1	AIAD_MOUSE	O93127 balanus amp
37	505.5	22.1	562	1	AIAD_MOUSE	P97714 mus musculus
38	504	22.0	451	1	DADR_XENLA	P42289 xenopus lae
39	503.5	22.0	561	1	DADR_RAT	P23944 ratius norv
40	503	21.9	572	1	AIAD_HUMAN	P25100 homo sapien
41	492.5	21.5	457	1	BDOR_XENLA	P42290 xenopus lae
42	492.5	21.5	539	1	D0P2_DROME	O24563 drosophila
43	490.5	21.4	385	1	BIAR_XENLA	O42574 xenopus lae
44	490.5	21.4	477	1	OAR_HELVI	O25188 heliothis v
45	489.5	21.4	477	1	BDOR_HUMAN	P21918 homo sapien

ALIGNMENTS

```

RESULT 1
ID      5H6_HUMAN          STANDARD:      PRT:      440 AA.
AC      P50406; Q13640;
DT      01-OCT-1996 (rel. 34, Created)
DT      01-OCT-1996 (rel. 34, Last sequence update)
DE      20-AUG-2001 (rel. 40, Last annotation update)
DE      5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).
GN      HTR6.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Striatum;
RX      MEDLINE=96102917; PubMed=8522988;
RA      Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RT      Sibley D.R., Roth B., Hamblin M.W.;
RT      "Cloning, characterization, and chromosomal localization of a human
RT      5-HT6 serotonin receptor.";
RL      J. Neurochem. 66:47-56(1996).
RN      [2]
RP      SEQUENCE OF 215-280 FROM N.A.
RC      TISSUE=Striatum;
RX      MEDLINE=95385798; PubMed=7656980;
RA      Ulmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RT      "Expression of serotonin receptor mRNAs in blood vessels.";
RT      FEBS Lett. 370:215-221(1995).
CC      -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC      5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
CC      AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC      THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC      CYCLASE. IT HAS A HIGH AFFINITY FOR TRICICLIC PSYCHOTROPIC DRUGS.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN SEVERAL HUMAN BRAIN REGIONS. MOST
CC      PROMINENTLY IN THE CAUDATE NUCLEUS.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb.ch/announce/
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CC      -----
DR      EMBL: L41147; AAA92622.1; -
DR      EMBL: 249119; CAA88929.1; -
DR      GCRDB: GCR_1062; -
DR      GCRDB: GCR_1885; -
DR      MIM: 601109; -
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR01102; 5HT6RECEPTR.
DR      PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.

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RESULT	2
5H6_MOUSE	
ID	5H6_MOUSE
AC	STANDARD;
DT	PRT; 440 AA.
DD	20-AUG-2001 (Rel. 40, Created)
DD	20-AUG-2001 (Rel. 40, Last sequence update)
DD	20-AUG-2001 (Rel. 40, Last annotation update)
DE	5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).
GN	5HT6.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID	10090;

Query Match	86.88;	Score 1989;	DB 1;	Length 440;
Best Local Similarity	87.66;	Pred. No. 2,7e-118;		
Matches 387;	Conservative 15;	Mismatches 36;	Indels 4;	Gaps

QY	1	MVEPGEPTANSTPAMGAGPPSPAGSGGVAALCVIALTPAANSLLIALICTPALRNT	60
	1	MVEPGEVNSTSTPAMGCGPPAPAGSGGVAALCVIITLTPAANSLLIALICTPALRNT	60
Db			
QY	61	SNFPLVLSFTSDIMVGVIVMPAPALINLVGKRWVLAIRGLCLIMTAFEDWCCSASILNCLT	120
Db	61	SNFPLVLSFTSDIMVGVIVMPAPALINLVGKRWVLAIRGLCLIMTAFEDWCCSASILNCLT	120
QY	121	SLDRYLLILSPRLKRLKMTPLRALATLVIGAMSLAALASFLPILLLGHWELHGAKRISAFPGQC	180
Db	121	SLDRYLLILSPRLKRLKMTAPRALATLVIGAMSLAALASFLPILLLGHWELHGAKRISAFPGQC	180
QY	181	RLIASLPEVLVASCSTFLFDSGALICFTYCRILLAAKRAQVAVASLTITGMAS--QASSETIQ	238
Db	181	RLIASLPEVLVAVASGVEFFELDSGALICFTYCRILLAAKRAQVAVASLTITGMATGAQLETIQ	240
QY	239	VPRPRGVSADSRRLATKHSRKALKAKLTLLGLLGMFEVTVMLPFFVAVIVAVVDCIS	298

Db 241 VPRTPPGMESADSRRLTKHSHKALKASLTLLGILSMFEVTLPEFVASIAQAVDCIS 300
 QY 299 PGFEDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRQASIASLSTSHS 358
 Db 301 PGFEDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRQASIASLSTSHS 360
 QY 359 GPRPGSLQOVLPLPPSDSDSDAGSGSSGLRLTAQLLPGCATODPPLTRAAAV 418
 Db 361 GARGSLQOVLPLPPSDSDSDAGSGSSGLRLTAQLLPGCATODPPLTRAAAV 418
 QY 419 NFEVNDPAPELRPHPLGPTN 440
 Db 419 NFEVNDPAPELRPHPLGPTN 440
 RESULT 3
 SH6_RAT STANDARD; PRT: 436 AA.
 AC P31388;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)
 GN HTR6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Striatum;
 RX MEDLINE=93196608; PubMed=7680751;
 RA Monsma F.J., Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;
 RT "Cloning and expression of a novel serotonin receptor with high
 RT affinity for tricyclic psychotropic drugs.";
 RL Mol. Pharmacol. 43:320-327(1993).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277562; PubMed=8389146;
 RA Ruat M., Traifort E., Ariang J.-M., Tardivel-Lacombe J., Diaz J.,
 RA Leurs R., Schwartz J.-C.;
 RT "A novel rat serotonin (5-HT6) receptor: molecular cloning,
 RT localization and stimulation of cAMP accumulation.";
 RL Biochem. Biophys. Res. Commun. 193:268-276(1993).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTAR;
 RA Martial R.;
 RT Submitted (xxx-1993) to the EMBL/Genbank/DBJ databases.
 RT -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
 RT 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
 RT AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
 RT THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
 RT CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS.
 RT -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 RT -1- TISSUE SPECIFICITY: LOCALIZED EXCLUSIVELY IN THE CENTRAL NERVOUS
 RT SYSTEM, PREDOMINANTLY IN THE CORPUS STRIATUM BUT ALSO IN VARIOUS
 RT LIMBIC AND CORTICAL REGIONS.
 RT -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: I03202; AAA0618.1; -
 DR EMBL: S62043; AAB26908.1; -
 DR EMBL: L19656; AAA0611.1; -
 DR GCRDB; GCR_0723; -

DR GCRDB; GCR_0719; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PRO00237; GPCRHOPOPSN.
 DR PRINTS: PRO1102; 5HTRECEPT.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1;
 DR PROSITE: PS00262; G_PROTEIN_REC_P1.2;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 34
 FT TRANSMEM 35 57
 FT DOMAIN 58 64
 FT TRANSMEM 65 85
 FT DOMAIN 86 100
 FT TRANSMEM 101 122
 FT DOMAIN 123 144
 FT TRANSMEM 145 166
 FT DOMAIN 167 184
 FT TRANSMEM 185 208
 FT DOMAIN 209 265
 FT TRANSMEM 266 290
 FT DOMAIN 291 320
 FT TRANSMEM 321 436
 FT CARBOHYD 9 9
 FT DISULFID 99 180
 FT CONFLICT 57 57
 FT CONFLICT 336 436
 SQ SEQUENCE 436 AA; 46922 MW; 6BC00F6A3CBAB5F4 CRC64;
 Query Match 73.2%; Score 1678; DB 1; Length 436;
 Best Local Similarity 91.7%; Pred. No. 9, 1e-99;
 Matches 322; Conservative 6; Mismatches 23; Indels 0; Gaps 0;
 QY 1 MVEPPTANSTPWAGCAPSGGWAALCVYIALTAANSLILALICTOPALRNT 60
 Db 1 MVEPPTANSTPWAGCAPSGGWAALCVYIALTAANSLILALICTOPALRNT 60
 QY 61 SNFEVLSLFTSDLMVGLVWPPAMALNLYGRWLAARGLCLMTAFVDCSASTLNLCL 120
 Db 61 SNFEVLSLFTSDLMVGLVWPPAMALNLYGRWLAARGLCLMTAFVDCSASTLNLCL 120
 QY 121 SLDRYLLIISPLRYKRLMTPLRALALVLAWSLAALASFLPLLGHEIGHARPPVGGC 180
 Db 121 SLDRYLLIISPLRYKRLMTPLRALALVLAWSLAALASFLPLLGHEIGHARPPVGGC 180
 QY 181 RLILASLPEVLVAGLTFPLPSAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240
 Db 181 RLILASLPEVLVAGLTFPLPSAICFTYCRILLAARKQAVASLTGTGASQSEFLQVP 240
 QY 241 RTPRPGVESADSRRLTKHSHKALKAKITGILGMEFVTLPEFVANITVQAVDCISPG 300
 Db 241 RTPRPGVESADSRRLTKHSHKALKAKITGILGMEFVTLPEFVANITVQAVDCISPG 300
 QY 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRQASIASLSTSHS 351
 Db 301 LFDVLTWLGYNSTNMPITPLFMDFKRALGFLPCRCRQASIASLSTSHS 351
 RESULT 4
 ID BIAR_MOUSE STANDARD; PRT: 466 AA.
 AC P34971;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE BETA-1 ADRENERGIC RECEPTOR.

GN ADRB1 OR ADRB1R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/SV;
 RA MEDLINE=93372116; PubMed=8395893;
 RT Jasper J.R., Link R.E., Chruscinski A.J., Kobilka B.K., Bernstein D.;
 RL "Primary structure of the mouse beta 1-adrenergic receptor gene";
 CC Biochim. Biophys. Acta 1178:307-309(1993).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
 CC APPROXIMATIVELY EQUAL AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; LI0084; AAA02929.1; -
 DR PIR; S36794; S36794.
 DR HSSP; P07700; IDEP.
 DR GCRDB; GCR_0578; -
 DR MGD; MGT:87937; Adrb1.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR00561; ADRENERGICBLR.
 DR PRINTS; PR01103; ADRENERGICR.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 59
 FT TRANSMEM 60 83
 FT DOMAIN 84 96
 FT TRANSMEM 97 120
 FT DOMAIN 121 131
 FT TRANSMEM 132 155
 FT DOMAIN 156 175
 FT TRANSMEM 176 199
 FT DOMAIN 200 221
 FT TRANSMEM 222 245
 FT DOMAIN 246 314
 FT TRANSMEM 315 338
 FT DOMAIN 339 345
 FT TRANSMEM 346 369
 FT DOMAIN 370 401
 FT CAROYHD 15
 FT DISULFD 131
 FT LIPID 381
 FT MOD_RES 296
 FT MOD_RES 301
 FT MOD_RES 401
 FT MOD_RES 401
 FT SEQUENCE 466 AA; 50479 MW; 753CD44C42BC9211 CRC64;

Query Match 25.8%; Score 591.5; DB 1; Length 466;
 Best Local Similarity 35.9%; Pred. No. 16e-30;
 Matches 158; Conservative 63; Mismatches 154; Indels 65; Gaps 17;
 7 PTANSTPAWGAGPPSAPGSGCWAA--ALCVIALTAANSLTALICTOPALRNTSNF 63

Db 38 PPSALPPASEG--SAPLSQOMTAGMGLVALLVLLVGNVLVYIAIAKTPRLQTLTNL 95
 QY 64 FLVSLFTSDMLVGLVYVPPAMALNAYGRVNLARGICLMTAFDPVCCSASILNLCISLD 123
 Db 96 FIMSLASADLVGLVLPFCATVYVGRMVEGSPFCGLMTSDVLCVTASIEFLCVIALD 155
 QY 124 RYLLISPLKYKLRMPRLRALVLGAMSLAALASFLPLLGN--HELGHARPPV--PGQ 179
 Db 156 RYLAISPFERYQSILTRARALVCTYWAISALVSFLPIIMHMMWRASDPAKRCYNDPK 215
 QY 180 CRLASLPELVYVSGLEFLPSAICFTYRILLARKAVQVQAS---LTGMAQAS-- 234
 Db 216 CDVYTNRAIVASSVSEVFLCMAFVLYVREKQYKIDSCERRFLGGPARPPSP 275
 QY 235 ETLQVPTPRPGVESADSR-----RLATKSRKALKAKATLIGILMGFTVLPPEFVA 287
 Db 276 EPSPSPGPAPADSLANGRSKRPRSLVALRQKALK--TLGIIMGVTTLCMLPEFLA 332
 QY 288 NIYQAV--CCISPGLEDVLTWLGYSNMPPIY---PLEMRDFKALGRFLPCPR---C 340
 Db 333 NVKAFHRDLVDPRLVFENMLGVANSAPNPITYCRSP---DFRAAFRLCCARRAAC 388
 QY 341 PREROASLASPLRTSHSGPRGLS--LQOVLPPLP--PDSDSDDAG----- 385
 Db 389 RR-----RAAH-GDRPASGLARACPPSPGAPSDDDDDAGTTPPARLLEPW 436
 QY 386 ---SGSSSGLRLTAQLLPG 402
 Db 437 TCGNGGTTVSDSDSLDEPG 456

RESULT 5
 BLAR_CANFA STANDARD; PRT; 473 AA.
 ID BLAR_CANFA
 AC P79148;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BETA-1 ADRENERGIC RECEPTOR.
 GN ADRB1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97364078; PubMed=9220370;
 RA Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascieri M.A.,
 RA Fong T.M.;
 RT "Molecular cloning of the dog beta 1 and beta 2 adrenergic
 RT receptors";
 RL J. Recept. Signal Transduct. Res. 17:599-607(1997).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
 CC APPROXIMATIVELY EQUAL AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; U73207; AAB93648.1; -
 DR HSSP; P07700; IDEP.
 DR GCRDB; GCR_1183; -

DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PRO00237; GPCR_RHODOPSIN.
 DR PRINTS: PRO0561; ADRENRCGBLAR.
 DR PRINTS: PRO1103; ADRENRCGBLAR.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 KM DOMAIN 1 59
 FT TRANSMEM 60 83
 FT DOMAIN 84 96
 FT TRANSMEM 97 120
 FT DOMAIN 121 131
 FT TRANSMEM 132 155
 FT DOMAIN 156 175
 FT TRANSMEM 176 199
 FT DOMAIN 200 221
 FT TRANSMEM 222 245
 FT TRANSMEM 246 322
 FT TRANSMEM 323 346
 FT TRANSMEM 347 353
 FT TRANSMEM 354 377
 FT DOMAIN 378 473
 FT CARBOHYD 15 15
 FT DISULFID 131 209
 FT MOD.RES 309 309
 FT LIPID 389 389
 FT SEQUENCE 473 AA: 50060 MW: 361357.77DF9DDBD7E CRC64;

Query Match 25.6%; Score 587.5; DB 1; Length 473;
 Best Local Similarity 35.6%; Pred. No. 2.8e-30;

*Matches 160; Conservative 67; Mismatches 152; Indels 71; Gaps 19;

QY 1 MWPEGPANTSPWAGGPPSAPAGSGWVAA---ALCVIATLAANSLILICTQPAL 57
 DB 33 LVP-ASPSASPLAPISSEGP--APLSQWTFAGIGILMALIVLLIVAGNVIAIAIATPRL 89
 QY 58 RMTSNFELSLFTSDMLVGLVMPMLNALYGRWLVANGICLILMTAFVYMCSSASILNL 117
 DB 90 QLTNLFNLSLASADLVGLVMPGATVYMRGWEYSGFLCELTWSVDVLCVTASIEYL 149
 QY 118 CUISLDRLYLISPLRYKRLMTPLRALALVLCAMSLAALASFLPLLGLMHELG--HARPP 175
 DB 150 CYTALDRYLAITAFPRYQSLTRARARALVCYMAISALVSEPLITIMHWRAGGDARRC 209
 QY 176 V--PGQCRLLASLPVLVASGLTFELPSGALCTCYCRILLAKKQAVOYAS---LTTGM 229
 DB 210 YNDPKCDEVTNRKAVAIASSVSEYVPLCIMAFLVLRVFRQAKQKIDSCERRFLGSP 269
 QY 230 A-----SQASETLOVPTPRGVS--ADSR-----RLATKSRKALAKLTLGLL 273
 DB 270 APPAPAPPAAPAPAPAPSPAAAPALANGVRRRSRLVALREQALK--TLGIT 326
 QY 274 LGMEFTWMLPEFVAVVQAV--CDCISPLGLEVDYTLVGLYCSNPNPITY---PLFMDFKR 329
 DB 327 MGVTITCLWLPFLANVYKAFHRDLVPRDLRFVFNMLGYANSAFNPLITTCRSP----DFKR 382
 QY 330 ALGRFLPCRCPRERQASLASPSLRTSH--SGPRPLSLQOVLPLPLP-----PDSDDSDS 382
 DB 383 AFQRLLCAR-----RAARGSHGAGDPP-----RAAPSPSPCAASDDDDDDDD 426
 QY 383 DAGSGSSGLRLTAQLLP-----GEATOD 407
 DB 427 DAGAG--AGAAPPARLLERWAGCNGGAAD 454

RESULT 6
 BLAR_RAT STANDARD; PRT: 466 AA.
 AC PI8090;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE BETA-1 ADRENERGIC RECEPTOR.
 GN ADRB1 OR ADRB1R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90350633; PubMed=1695899;
 RA Machida C.A., Bunzow J.R., Seales R.P., van Tol H.H.M., Testar B.,
 RT Neve K.A., Teal P., Nipper V., Civelli O.;
 RT "Molecular cloning and expression of the rat beta 1-adrenergic
 RT receptor gene.";
 RL J. Biol. Chem. 265:12960-12965(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90356399; PubMed=2167473;
 RA Shimomura H., Terada A.;
 RT "Primary structure of the rat beta-1 adrenergic receptor gene";
 RL Nucleic Acids Res. 18:4591-4591(1990).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
 CC APPROXIMATIVELY EQUAL AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
 CC PHOSPHORYLATION BY BETA-ADRENERGIC KINASE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: J05561; AAA0792.1; -
 DR EMBL: D00634; BAA00527.1; -
 DR PIR: A36618; A36618.
 DR PIR: S12591; S12591.
 DR HSSP: P07700; IDEP.
 DR GCRDB: GCR_0126; -
 DR GCRDB: GCR_0127; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PRO00237; GPCR_RHODOPSIN.
 DR PRINTS: PRO0561; ADRENRCGBLAR.
 DR PRINTS: PRO1103; ADRENRCGBLAR.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT TRANSMEM 1 59
 FT DOMAIN 60 83
 FT TRANSMEM 84 96
 FT TRANSMEM 97 120
 FT DOMAIN 121 131
 FT TRANSMEM 132 155
 FT DOMAIN 156 175
 FT TRANSMEM 176 199
 FT DOMAIN 200 221
 FT TRANSMEM 222 245
 FT TRANSMEM 246 314
 FT TRANSMEM 315 338
 FT TRANSMEM 339 345
 FT TRANSMEM 346 369
 FT DOMAIN 370 466
 FT CARBOHYD 15 15
 FT DISULFID 131 209
 FT LIPID 381 381

FT MOD_RES 296 296 PHOSPHORYLATION (BY CARK) (POTENTIAL).
 FT MOD_RES 301 301 PHOSPHORYLATION (BY CARK) (POTENTIAL).
 FT MOD_RES 401 401 PHOSPHORYLATION (BY CARK) (POTENTIAL).
 FT CONFLICT 162 162 L -> S (IN REF. 2).
 FT CONFLICT 267 267 T -> S (IN REF. 2).
 SQ SEQUENCE 466 AA; 50471 MW; 2955CB024944A12B CRC64;

Query Match 25.6%; Score 586.5; DB 1; Length 466;
 Best Local Similarity 35.5%; Pred. No. 3.2e-30;
 Matches 156; Conservative 63; Mismatches 156; Indels 65; Gaps 16;

QY 7 PTANSPWAGGPPSAPGSGGWVAA--ALCVVIALTAANSLLILICQPALRNTSNF 63
 DB 38 PPSASLPAPSEG--SAPLSQMTAGMGLLALLVLLVGNVIAIAKTPRIQTLTNL 95
 QY 64 FLVSLFTSDLMGLVMPAMALYGRVYLAGLCLMTAFDVMCCSASILNLCISLD 123
 DB 96 FIMSLASADLVMLGLVPGATIVMGREYGSFCELMTSVDVLCVTASIEFLVIALD 155
 DB 124 RYLLISPLRYKLRMTPLRALVYLGANSIALASFLPLILGW--HELGHARPPV--PGQ 179
 DB 156 RYLAITLPRYOSLLTRARARALVCTVMAISALVSLPLIMHWRABESDEARCYNDPKC 215
 QY 180 CRLLASLPVYVAGSLTFPLPSGALCYCRILLARKOAVOYAS--LTGMASQAS 234
 DB 216 CQEVTRAAVAIASVSVFYPLCIMAFLVLRERAKOVKKIDSCERREFLGPPPPSP 275
 QY 235 ETLQVPRPRPGVESADSR-----RLATKHSRKALKKALGLLGLMFFVYMLPEFVA 287
 DB 276 AVSPSPGPPRADSLANGRSSKRPSRLVALRQKALK--TLGIMGVFTLCWLPFLA 332
 QY 288 NIVQAN--CCGISPLGLFDVLWLYGCSYTNMPTIY---PLFMRFKALGRFLCPR---C 340
 DB 333 NVYKAPHRDLVPRDLVFEFNWGLYANSAPNPIIYCRSP---DFKRAFQRLLOCARRAC 388
 QY 341 PERQASLASPLRSTSHSGPRPLS--LQOVLPLPLP--PDSDSDDAG----- 385
 DB 389 RR-----RAAH--GDRPRASGLARAGPPSPGAPSDDDDDACATPPARLLERW 436
 QY 386 ---SGSSGLRLTQALLPLG 402
 DB 437 AGCNGGTTVDSDDSLDEPG 456

RESULT 7
 BIAR_FELICA STANDARD: PRT: 474 AA.
 QY 20-AUG-2001 (Rel. 40, Created)
 DB 20-AUG-2001 (Rel. 40, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BETA-1 ADRENERGIC RECEPTOR.
 GN ADRB1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cully D.F., Tremml G., Zachwieja S.;
 RT "Felis domesticus beta adrenergic receptor subtype 1.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE ACTION OF G
 INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
 APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC - PM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
 PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
 SIMILARITY).
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC or send an email to license@sdb-sdb.ch).

DR EMBL: AF192344; AAF04303.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1. 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PRINTS: PRO0561; ADRENERGIC.
 DR PRINTS: PRO103; ADRENERGIC.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1.1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECIP_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 59
 FT TRANSMEM 60 83
 FT DOMAIN 84 96
 FT TRANSMEM 97 120
 FT DOMAIN 121 131
 FT TRANSMEM 132 155
 FT DOMAIN 156 175
 FT TRANSMEM 176 199
 FT DOMAIN 200 221
 FT TRANSMEM 222 245
 FT DOMAIN 246 321
 FT TRANSMEM 322 345
 FT DOMAIN 346 352
 FT TRANSMEM 353 376
 FT DOMAIN 377 474
 FT CARBOHYD 15 15
 FT DISULFID 131 209
 FT MOD_RES 308 308
 FT LIPID 388 388
 SQ SEQUENCE 474 AA; 50532 MW; 2FC97DE4CFB7C3F CRC64;

Query Match 24.9%; Score 571; DB 1; Length 474;
 Best Local Similarity 34.7%; Pred. No. 3.1e-29;
 Matches 162; Conservative 66; Mismatches 167; Indels 72; Gaps 20;

QY 1 WYPERPTANSPWAGGPPSAPGSGGWVAA--ALCVVIALTAANSLLILICQPAL 57
 DB 33 LVP-ASPSASPLPTISEGP--APLSQMTAGIGLMLALLVLLVGNVIAIAKTPRL 89
 QY 58 RMTNSFLVSLFTSDLMGLVMPAMALYGRVYLAGLCLMTAFDVMCCSASILN 117
 DB 90 QTLNLEIMSLASADLVMLGLVPGATIVMGREYGSFCELMTSVDVLCVTASIEFL 149
 QY 118 CLISDRYLLISPLRYKLRMTPLRALVYLGANSIALASFLPLILGW--HELGHARPP 175
 DB 150 CVIALDRYLAITSPPRYOSLLTRARARALVCTVMAISALVSLPLIMHWRABESGARRC 209
 QY 176 V--PGOCLLASLPVYVAGSLTFPLPSGALCYCYCRILLARKOAVOYAS--LTTGM 229
 DB 210 YNDPCCQEVTRAAVAIASVSVFYPLCIMAFLVLRERAKOVKKIDSCERREFLSGP 269
 QY 230 ASOASETLQVPRPRPGVESADS-----RLATKHSRKALKAKLITLITL 273
 DB 270 ARPPSPA-PAGSPSPRAATAAAAAAAPLANGRIKKRRPSRLVALREKALK--TLGIT 325
 QY 274 LGMFVYMLPEFVAVIVAV--CDCISPLGLFDVLWLYGCSYTNMPTIY---PLFMRDKR 329
 DB 326 MGVFLCWLPEFLAVVAVAFHDLVPRDLVFEFNWGLYANSAPNPIIYCRSP---DFRK 381
 QY 330 ALGRFLPCPCPRERQASLASPLTSH--SGPRGLS--LQOVLPLPLP--PDSDS 382
 DB 382 AFORLL---CFARRAA-----RGHAAAGDRPRASGLCPGTPPSPGASDEDODD 430
 QY 383 DAGSGSSGLRLTQALLPLGATQDPLPTRAAAAVNFNID-PAEP 428

DB 431 DVGAMP-----PARLEPWACNG-----GAAADSDSLDEPGR 466

RESULT 8

BLAR_MACMU STANDARD: PRT: 480 AA.

AC P47899;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE BETA-1 ADRENERGIC RECEPTOR.

GN ADRL.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI_Taxid=9544;

RP SEQUENCE FROM N.A.

RP MEDLINE=95078456; PubMed=7987008;

RT "The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and comparison of the flanking sequences with the rat beta 1-adrenergic receptor gene.";

RT DNA Seq. 4:231-241(1994).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: X75540; CAA53228.1; -

DR HSSP: P07700; IDEP.

DR GCRDB: GCR_1746; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODOPSN.

DR PRINTS: PR00561; ADRENERGICBLAR.

DR PRINTS: PR01103; ADRENERGICR.

DR PROSITE: PS00337; G_PROTEIN_RECP_FL_1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

DR Multigene family; Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 59

FT TRANSMEM 60 83

FT DOMAIN 84 96

FT TRANSMEM 97 120

FT DOMAIN 121 131

FT TRANSMEM 132 155

FT DOMAIN 156 175

FT TRANSMEM 176 199

FT DOMAIN 200 221

FT TRANSMEM 222 245

FT DOMAIN 246 328

FT TRANSMEM 329 352

FT DOMAIN 353 359

FT TRANSMEM 360 383

FT DOMAIN 384 480

FT CARBOHYD 15

FT DISULFID 131

FT MOD_RES 315

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD_RES 415 415 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT LIPID 395 395 PALMITATE (BY SIMILARITY).

SO SEQUENCE 480 AA: 51608 MW: 25CB18PA03128084 CRC64:

Query Match 24.6%; Score 563.5; DB 1; Length 180;

Best Local Similarity 34.5%; Pred. No. 9, 1e-29;

Matches 149; Conservative 62; Mismatches 166; Indels 55; Gaps 14;

QY 1 MWPEPPTANSTPMAGCGPPSAPGSGWVA--ALCVYIALTAANSLLIALICTOPAL 57

DB 33 LVP-ASPPASLLPPASEGP--EPLSQQWTAGMGLMALIVLLVAGNVIVIAIAIAPRL 89

QY 58 RMTSNFELVSLFSDMLVGLVWPMALNAIVGRWLANGGLCLVAFVPMCCSASILNL 117

DB 90 QYTLNLFMSLASDLVWGLVVPFGATVYWGKRWYGSFCEELWTSVYLCTYASTIEL 149

QY 118 CLISLDRLYLILSPYKRYKMTPLRALALVLGMSIALASFLPLDGLV--HELGHARPP 175

DB 150 CVIALDRLYLILSPYKRYKMTPLRALALVLGMSIALASFLPLDGLV--HELGHARPP 209

QY 176 V--PGOCLLASLPEVLYVAGSLTFELPSCAICFTYCRILIAARKQAVQAS---LTGM 229

DB 210 YNDPKCCDEVTRAVAYAIASVSVFYPLCIMAFLVLRVEREQKYKIDQCERRFLGSP 269

QY 230 ASQASET-----LQYPRPRGVEASDS-----RLATKHSRKALKAK 267

DB 270 ARPPSPSPSPSPSPVAPPPGPPRAAAATTPALVNGRAGKRSPRLVALRQAKLK-- 327

QY 268 LTLGLILGFEVYTLPEFVANIQAQV--CDICSPGLPDLVTLGYCSTNMPITV---PLP 323

DB 328 -FLGILMGVFTLCWLPFLFANVAKARRELVPRLFEVFNWLGYSANSPNLIYCRSP-- 384

QY 324 MDPFKALRFLPCPCPRERQASLASPSLRTHSHSPRGCLSLQVLLPLP--PDSDSS 382

DB 385 --DFRNAFORLLCCARRAARRHAHGRPRASGLARPG-----PPSPGASDIDD 435

QY 383 DAGSGSSGLRL 394

DB 436 DDVVGATGPRL 447

RESULT 9

BLAR_PIG STANDARD: PRT: 468 AA.

AC Q28998; O46575;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUL-1998 (Rel. 38, Last annotation update)

DE BETA-1 ADRENERGIC RECEPTOR.

GN ADRL.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_Taxid=9823;

RP SEQUENCE FROM N.A.

RP MEDLINE=98318327; PubMed=9655595;

RP Cao H., Bidwell C.A., Williams S.K., Liang W., Mills S.E.;

RP "Nucleotide sequence of the coding region for the porcine beta1-adrenergic receptor gene.";

RP J. Anim. Sci. 76:1720-1721(1998).

RP (2)

RP SEQUENCE OF 101-468 FROM N.A.

RP TISSUE=Heart;

RA McNeel R.L., Mersmann H.J.;

RA Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.

RT FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS

CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
 CC SIMILARITY). BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY:-----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF042454; AAB97525.1; -
 DR EMBL: U56425; AAC06330.1; -
 DR HSSP: P07700; IDEP.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00561; ADRENERGICBLAR.
 DR PRINTS: PR01103; ADRENERGICR.
 DR PROSITE: PS00237; G-PROTEIN-RECEP_FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN-RECEP_FL2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 KW DOMAIN 1 59
 FT TRANSMEM 60 83
 FT DOMAIN 84 96
 FT TRANSMEM 97 121
 FT DOMAIN 122 132
 FT TRANSMEM 133 153
 FT DOMAIN 154 176
 FT TRANSMEM 177 197
 FT DOMAIN 198 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 315
 FT TRANSMEM 316 336
 FT DOMAIN 337 347
 FT TRANSMEM 348 368
 FT DOMAIN 369 468
 FT CARBOHYD 15 15
 FT DISULFID 131 208
 FT LIPID 382 382
 FT CONFLICT 173 173
 FT CONFLICT 316 316
 FT CONFLICT 326 328
 FT CONFLICT 448 448
 FT CONFLICT 458 458
 FT CONFLICT 463 464
 FT SEQUENCE 468 AA; 50098 MW; 93C3AE78B703225 CRC64;
 Query Match 24.4%; Score 559; DB 1; Length 468;
 Best Local Similarity 33.3%; Pred. No. 1.7e-28;
 Matches 149; Conservative 67; Mismatches 160; Indels 72; Gaps 15;
 Oy 1 WPEEGPTANSPRA-----WGAGPPSAPGSGGWAALCVIALTAANSLITL 50
 Db 33 LVPAASPASULTPASEGVSQSOQNTAG-----MGLMALVLLIVAGNVLVIA 82
 Oy 51 ICTOPALRNTSNFLVSLFTSDLVAGLVVMPAMALAYGRVNLARGCLMTAFDVMCC 110
 Db 83 IAKTPRLQTLNLFMSLASADLVGLVPGATIVVWGRNEYSFCELMTSVDVLCV 142
 Oy 111 SASIINCLISIDRYLLISPLRYLRLMTPLRALVIGMSLAALASFLPLLIGW--HE 168
 Db 143 TASITTLVIALDRYLAITSFQYOSLT-RAARALVCTVMAISALVSFLPIIMMMWRK 201
 Oy 169 LGHARPPV--PQCGRLASLPVLVAGTFLPSGATCFCTCRILLAKRQAVASIT 226
 Db 202 GAEARRCNDKCCDFVYNNRAVLAASVVSFVPLCIAMAFVLRVREKQVKRKIDSC 261
 Oy 227 ---TGMAQSASETLQVPTPRGVESA-----DSRLATKHSRKALKATLTGI 272

Db 262 RFLGSPARPSPSPSPGSLPAAAAAPVANGRTSKRRSRRLVALREKALK---TLGI 318
 Oy 273 LIGMEFVTLPEFVAVIYQAV-CDGISPGLEVDLTMIGYCNSTMPN1Y---PLFMRDK 328
 Db 319 IMGVFLCMLPEFLAVVAFHFDLVPDRLEFVFNMLGANSFN1YICRSP-----DR 374
 Oy 329 RALGRFLPCRCRERQASLASPSLFTSHSGPPGLSLQOVLPLP-----PDSDSDSA 384
 Db 375 KAFQRLICCAR-----RVARGSCAAAGDGPRAAGCLAVARPPSPGAASDDDEEDV 427
 Oy 385 GSGSSGLRLTAQLLP-----GEAROD 407
 Db 428 GAAP-----PAPLEPMAGYNGCAARD 449
 RESULT 10
 B3AR CANFA STANDARD; PRT: 405 AA.
 AC 002662; Q9TTT2;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE BETA-3 ADRENERGIC RECEPTOR.
 GN ADRA3 OR B3AR.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN NCBI_TaxId=9615;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99095920; PubMed=9881593;
 RA Lenzen G., Pietri-Rouxel F., Drumare M.F., Amiard A., Guillot S.,
 RA Archimbaud P., Strosberg A.D.;
 RT "Genomic cloning and species-specific properties of the recombinant
 RL canine beta3-adrenoceptor";
 RN Eur. J. Pharmacol. 363:217-227(1998).
 RP SEQUENCE FROM N.A.
 RA Thompson G.M., Kelly L.J., Candellore M.R.;
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
 CC THERMOGENESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: U92468; AAB51068.1; -
 DR EMBL: AF200597; AAF08307.1; -
 DR HSSP: P07700; IDEP.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00563; ADRENERGICBLAR.
 DR PRINTS: PR01103; ADRENERGICR.
 DR PROSITE: PS00237; G-PROTEIN-RECEP_FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN-RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 36
 FT TRANSMEM 37 63
 FT DOMAIN 64 72
 FT TRANSMEM 73 91
 FT DOMAIN 92 111
 FT TRANSMEM 112 133


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DB 150 CVALDRLATSPFRQSLTTRARALVCTYWAISALVFLPIFOMWMDADAKSRC 209
OY 176 --VPGOCRLIASLPEVLVAGSLTFLPSPGALCTFYCRILLAAKQAVOVAS---LTTGM 229
DB 210 YNDPECCDFIINGVAYATSSVSFVPLCIMAFLVLFVREAOQYKIDSCRRFLSGP 269
OY 230 ASQASELQVPRPRGVEASDR-----RLATKSRKALAKLTLGLLGMFFVTWL 282
DB 270 ARLPSRA-PSPGPPPLAATYVANGRRKRPRLVALREQALK---TLGITMGVFTLCWL 325
OY 283 PEFVANIYOVAV-CDGISPGLEFVLTWLGYSNTMNPITY---PLMRDFKALGRFLPCP 338
DB 326 PEFLANVVAHFHDVLDVDRLEFVFNMLGYANSAFNPIITVRSF---DFKAFQRLCCCA 381
OY 339 RCRERQASLASLSLTSHSGPPGSLQOVLPLPPSDSDSAGSGGSLRLTAQL 398
DB 382 R-----RAACGSHAAAGPPRALCLAVARPSFGAASDDDDDDDDVGAAPPVRL 434
399 LLP-----GEATQDDPLPTRAAAA 417
435 LEPWAGYNGGAANAASDSDSPDERSRACCA 462

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RESULT 12

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BIAR_HUMAN STANDARD: PRT: 477 AA.
ID P08588; O90K68; Q90K67;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA-1 ADRENERGIC RECEPTOR.
GN ADRA1 OR ADRA1R OR BIAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88068509; PubMed=2825170;
RA Friele T., Collins S., Daniel K.W., Caron M.G., Lefkowitz R.J.,
RA Koblika B.K.;
RT "Cloning of the cDNA for the human beta 1-adrenergic receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).
RN (2)
RX VARIANT ARG-389.
RX MEDLINE=99230291; PubMed=10212248;
RX Mason D.A., Moore J.D., Green S.A., Liggett S.B.;
RX "A gain-of-function polymorphism in a G-protein coupling domain of the
RX human beta1-adrenergic receptor.";
RX J. Biol. Chem. 274:12670-12674(1999).
RN (3)
RP VARIANTS GLY-49 AND ARG-389.
RX MEDLINE=99407229; PubMed=10477438;
RX Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.;
RX "Racial differences in the frequencies of cardiac beta(1)-adrenergic
RX receptor polymorphisms: analysis of c145A>G and c1165G>C.";
RX Hum. Mutat. 14:271-271(1999).
RN (4)
RP VARIANT GLY-49.
RX MEDLINE=20507547; PubMed=11052857;
RX Borjesson M., Magnusson Y., Hjalmarson A., Andersson B.;
RX "A novel polymorphism in the gene coding for the beta(1)-adrenergic
RX receptor associated with survival in patients with heart failure.";
RX Eur. Heart J. 21:1853-1858(2000).
CC -I- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
CC APPROXIMATELY EQUAL AFFINITY.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- PTM: HOMOLOUS DESENITILATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

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CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: J03019; AA051667.1; -
DR EMBL: AF169006; AAD53696.1; -
DR EMBL: AF169007; AAD53697.1; -
DR PIR: A39911; A39911.
DR HSP: P07700; IDEP.
DR GCRB: GCR_0048; -
DR MIM: 109630; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PRINTS: PR00561; ADRENERGICBIAR.
DR PRINTS: PR01103; ADRENERGICR.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate;
KW Polymorphism.
FT DOMAIN 1 59
FT TRANSMEM 60 83
FT DOMAIN 84 96
FT TRANSMEM 97 120
FT DOMAIN 121 131
FT TRANSMEM 132 155
FT DOMAIN 156 175
FT TRANSMEM 176 199
FT DOMAIN 200 221
FT TRANSMEM 222 245
FT DOMAIN 246 325
FT TRANSMEM 326 349
FT DOMAIN 350 356
FT TRANSMEM 357 380
FT DOMAIN 381 477
FT CARBOHYD 15 15
FT DISULFID 131 209
FT MOD_RES 312 312
FT MOD_RES 412 412
FT LIPID 392 392
FT VARIANT 49 49
FT VARIANT 389 389
FT SEQUENCE 477 AA; 51223 MW; 1D15E6390B5364B8 CRC64;
SQ
Query Match 24.3%; Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 2.3e-28;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;
OY 1 NVPEPGPTANSTPWAGAGPPAPGSGVAAALCVIALTAANSLTALICTOPALRNF 60
DB 33 LVPASPPASLILPPASESEPEPLSQOWTAGGLMALIVLIVAGNVLAVALAKTRLOTL 92
OY 61 SNEFLVSLFTSDLMVGLVMPMPAMINALYGRWVLAIGLCLMTADVMCCSASINLCIL 120
DB 93 TNLFTMSIASDLVGLVLPFGATIVVGRWEGSFCEIEMTSVDVLCVPASIEITLCVI 152
OY 121 SLDRVLLTSLPRYLRLMTPRALALVYGANSILASFLPLLGV--HEIGHAPPV-- 176
DB 153 ALDRYLAITSPPRYOSLTLTRAARGLVCTVVAISALVSFLPLMLHMAESDEARCYND 212
OY 177 PGQCLLASLPEVLVAGSLTFLPSPGALCTFYCRILLAAKQAVOVAS---LTTGMA 232
DB 213 PKCCDFVNRVAVLAASVSFVPLCIMAFLVLFVREAOQYKIDSCRRFLSGP 272

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[illegible]

FT	LIPID	SEQUENCE	361	361	PALMITATE (BY SIMILARITY).
SQ	SEQUENCE	405 AA:	43032 MW:	AZBAANAABE798ADS CXC64:	
	Query Match	24.1%;	Score 553.5;	DB 1:	Length 405;
	Best Local Similarity	34.3%;	Pred. No. 3.3e-28;		
	Matches 144;	Conservative 56;	Mismatches 165;	Indels 55;	Gaps 13;
OY	1	MVEERG-PANSTPMAGGPPSPAGSGGVAAALCVIALTVALTAAANSILIALICQPALARN	59		
Db	11	LTPWEDIFPLAANTMANASGLPGVPAAVALACALLALAVATVYGULLVVAIARTPRIQT	70		
OY	60	TSNEFLVSLEFSDLMVGLVMPAMPALNLGYRMVLARGCLGTAFDVMCCSASTLNDCL	119		
Db	71	MTNVEVTSLATADLVGLLVPPGATLTALTGHWPLGVTCGELMTSVDLVCYVASIEFLCA	130		
OY	120	ISLDRLYLTLSTLRKLRKMTPLRALALVUGAMSLAALSFLPBLLLGHNELG-----H	171		
Db	131	LAVDRYLAVNTPLNRGAIVLTRKRRAAAVAVLVVVVSAVAASFAPIMSKMRVGADAEARORCH	190		
OY	172	APPVPGCGCRLLASLPFLVLSAGLFPEFLPSGACICTYCRIILLAKROAVOV-----	222		
Db	191	SNPRC---CTFSMNPYALLSSVSFYFLPLVMLEVVARVFVDTRQLRLRELGRPPP	247		
OY	223	----ASLTGTMASQASETLOVPTRPQVESADSR--RLATKHISKALKAKVLGILIG	275		
Db	248	EESPAPNSGSGPPAG-----PYASPAGVPSEYGRPARLLPLRHRALIR--TLGLIMG	299		
OY	276	MEFWMLPEFFVANITVOAV--CDCISPGAIEDVLTWLGNCSTNPITY--PLFMDFKRA	330		
Db	300	TFTLWLMEFFVNVRVYALGRLVSGPFTFLALMWLGANSAPNPILTYCRSP-----DRISA	355		
OY	331	LGRLPLPCRPCRREROASLASPSLRTSHSGPRRGSLGQOVLPLPLPDSDSDSADSGSGSS	390		
Db	356	FRRL-L-C-RCPDEEHIAASP-----PRAPSAGPVLTLSPAPRQPPSLDGASCGLS	405		
	RESULT 15				
ID	B3AR_MOUSE	STANDARD:	PRT:	400 AA.	
AC	P25962; Q9Q298;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	BETA-3 ADRENERGIC RECEPTOR.				
OS	ADRB3 OR ADRB3R OR B3BAR.				
CS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBT_TaxID=10090;				
RN	[1]				
RN	SEQUENCE FROM N.A.				
RP	STRAIN-SWISS;				
RC	MEDLINE=92037534; PubMed=1718744;				
RX	van Spriksen A., Nahmias C., Krief S., Briand-Sutren M.-M.,				
RA	Strosberg A.D., Emorine L.J.;				
RA	"The promoter and intron/exon structure of the human and mouse beta				
RT	3-adrenergic-receptor genes.";				
RT	Eur. J. Biochem. 213:1117-1124(1993).				
RL	[3]				
RN	REVIEWSIONS, SEQUENCE FROM N.A.				
RP	MEDLINE=93279311; PubMed=8389293;				
RX	Evans B.A., Papaioannou M., Hamilton S., Summers R.J.;				
RA	"Alternative splicing generates two isoforms of the beta3-adrenoceptor				
RT					

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:08:55 ; Search time 17.53 Seconds
(without alignments)
1911.968 Million cell updates/sec

Title: US-09-826-509-449

Perfect score: 2292
Sequence: 1 MVEPEPTANSTRPWAGAGCP.....FNIDPAPELRPHPLGPTN 440

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2387	89.8	440	2	JC5520
2	1899.5	82.9	437	2	I57942
3	1678	73.2	436	2	JN0591
4	591.5	25.8	466	2	S36794
5	581	25.3	464	2	S12591
6	563.5	24.6	480	2	I53053
7	557	24.3	477	1	ORHUB1
8	554	24.2	405	2	S65459
9	552.5	24.1	400	2	S32804
10	552.5	24.1	446	1	DYHND1
11	551.5	24.1	400	2	A41679
12	551.5	24.1	400	2	A53281
13	547.5	23.9	363	2	I50475
14	543.5	23.7	418	2	G02953
15	538	23.5	446	2	I47217
16	535.5	23.4	386	2	S72168
17	535.5	23.4	428	2	A55044
18	533.5	23.3	487	1	DYRDL1
19	531	23.2	408	1	ORHUB2
20	531	23.2	414	1	ORHUB3
21	528.5	23.1	463	2	B56849
22	526.5	23.0	483	2	A25896
23	525	22.9	385	2	S68780
24	524.5	22.9	459	2	A56849
25	516	22.5	511	2	S44275
26	508	22.2	379	2	JC6178
27	507.5	22.1	560	2	A36731
28	504	22.0	451	2	I51659
29	503	21.9	572	2	I39369

ALIGNMENTS

30	500	21.8	450	2	A55886	dopamine receptor
31	499.5	21.8	501	2	JH0447	alpha-1A-adrenergic
32	492.5	21.5	457	2	I51660	dopamine D1B recep
33	489.5	21.4	477	1	DYHDS	dopamine receptor
34	487.5	21.3	444	2	C55886	dopamine receptor
35	487.5	21.3	475	2	A41271	dopamine receptor
36	487	21.2	465	2	I51661	dopamine D1C recep
37	487	21.2	515	2	JC1525	alpha-1B-adrenergic
38	486	21.2	515	2	A40491	alpha-1-adrenergic
39	482	21.0	359	2	A39008	histamine H2 recep
40	480.5	21.0	517	2	A45121	alpha-1B adrenergic
41	480	20.9	484	2	S58868	G protein-coupled
42	479.5	20.9	445	2	A48881	serotonin receptor
43	477	20.8	359	2	JH0449	histamine H2 recep
44	477	20.8	486	2	B55886	dopamine receptor
45	476.5	20.8	377	2	S68423	serotonin receptor

RESULT 1
JC5520
serotonin receptor 6 - human
N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)
C:Species: Homo sapiens (man)
C>Date: 02-Sep-1997 #sequence, revision 05-Sep-1997 #text, change 05-Nov-1999
C:Accession: JC5520
R:Kohen, R.; Metcalfe, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Melzack, R.; Neurochem. 66, 47-56, 1996
A:Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 se
A:Reference number: JC5520; MUID:96102917
A:Accession: JC5520
A:Molecule type: mRNA
A:Residues: 1-440 <KOH>
A:Cross-references: GB:I41147; NID:91162923; PIDN:AAA92622.1; PID:91162924
A:Experimental source: brain
C:Comment: This protein shows high affinity for several therapeutically important ant
C:Genetics:
A:Gene: HTR6
A:Map position: 1p35-36
A:Introns: 238/3; 291/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
F:28-51/Domain: transmembrane #status predicted <TM1>
F:65-88/Domain: transmembrane #status predicted <TM2>
F:100-123/Domain: transmembrane #status predicted <TM3>
F:143-166/Domain: transmembrane #status predicted <TM4>
F:185-208/Domain: transmembrane #status predicted <TM5>
F:266-289/Domain: transmembrane #status predicted <TM6>
F:298-321/Domain: transmembrane #status predicted <TM7>
F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 2287; DB 2; Length 440;
Best local similarity 99.8%; Pred. No. 8.6e-170;
Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVEPEPTANSTRPWAGAGCPSPAGSGGWAALCVYIALTAANSLIALICIQPALRNT 60
DB 1 MVEPEPTANSTRPWAGAGCPSPAGSGGWAALCVYIALTAANSLIALICIQPALRNT 60

QY 61 SNFELVSLFTSDLMVGLVMPAMALNAGRWLAGLCLMTAPVYMCCSASILNCL 120
DB 61 SNFELVSLFTSDLMVGLVMPAMALNAGRWLAGLCLMTAPVYMCCSASILNCL 120

QY 121 SDRYLLIISPLRYKRLRMTPLRALALVLGAMSLAALSFPLILGWHGSHARPVPGOC 180
DB 121 SDRYLLIISPLRYKRLRMTPLRALALVLGAMSLAALSFPLILGWHGSHARPVPGOC 180

QY 181 RLILASPLVLAASGLTFPLPSGAICFTYCRILLANKQAVQVSLTTGMASSQSEFLQVP 240
DB 181 RLILASPLVLAASGLTFPLPSGAICFTYCRILLANKQAVQVSLTTGMASSQSEFLQVP 240

QY 241 RTPRGVESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 |||||||
 Db 241 RTPRGVESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 QY 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360
 |||||||
 Db 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360
 QY 361 RFGSLQOVLPLPPDSDSGSGGLRLTAOLLPEATODPLPRAAAVNF 420
 |||||||
 Db 361 RFGSLQOVLPLPPDSDSGSGGLRLTAOLLPEATODPLPRAAAVNF 420
 QY 421 FNIDPAEELRPHPLGIPTN 440
 |||||||
 Db 421 FNIDPAEELRPHPLGIPTN 440

RESULT 2

7942
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 157942
 R:Monoma, F.J.
 Mol. Pharmacol. 43, 320-327, 1993
 A:Title: Cloning and expression of a novel serotonin receptor with high affinity for tri
 A:Reference number: 157942; MUID:93196608
 A:Accession: 157942
 A:Status: preliminary: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-437 <RDS>
 A:Cross-references: GB:L03202; NID:g294507; PIDN:AAA0618.1; PID:g294508
 C:Superfamily: vertebrate rhodopsin

Query Match 82.9%; Score 1899.5; DB 2; Length 437;
 Best Local Similarity 84.5%; Pred. No. 9e-140;
 Matches 376; Conservative 11; Mismatches 45; Indels 13; Gaps 4;

QY 1 WYPEPGPTANSTPAGAGPPAPSGGWAALCVIALTAANSLLIALICTOPALRNT 60
 |||||||
 Db 1 WYPEPGPTANSTPAGAGPPAPSGGWAALCVIALTAANSLLIALICTOPALRNT 60
 QY 61 SNFVLVSFTSDLMVGLVMPAMPALNLYGRWVLAAGLCCLMTAFDVMCCSASILNLCIL 120
 |||||||
 Db 61 SNFVLVSFTSDLMVGLVMPAMPALNLYGRWVLAAGLCCLMTAFDVMCCSASILNLCIL 120
 QY 121 SLDRLILSLPLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTAPAGQC 180
 |||||||
 Db 121 SLDRLILSLPLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTAPAGQC 180
 QY 181 RLASLSPVLVAGSLTFPLPSGAICFTYCRILIAARKQAVQASLTGASQASETLQVP 240
 |||||||
 Db 181 RLASLSPVLVAGSLTFPLPSGAICFTYCRILIAARKQAVQASLTGASQASETLQVP 240
 QY 241 RTRPRGESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 |||||||
 Db 241 RTRPRGESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 QY 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360
 |||||||
 Db 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCRCPRERQASLASPSLRTSHSGP 360
 QY 361 RFGSLQOVLPLPPDSDSGSGGLRLTAOLLPEATODPLPRAAAVNF 420
 |||||||
 Db 361 RFGSLQOVLPLPPDSDSGSGGLRLTAOLLPEATODPLPRAAAVNF 420
 QY 421 FNIDPAEELRPHPLGIPTN 440
 |||||||
 Db 421 FNIDPAEELRPHPLGIPTN 440
 QY 437 TVVNFVTDVSEPELRPHPLSSPVN 437

RESULT 3

JN0591
 serotonin receptor 6 - rat
 N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: JN0591
 R:Ruft, M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; S
 Biochem. Biophys. Res. Commun. 193, 268-276, 1993
 A:Title: A novel rat serotonin (5-HT6) receptor: molecular cloning, localization and
 A:Reference number: JN0591; MUID:93277562
 A:Accession: JN0591
 A:Molecule type: DNA
 A:Residues: 1-436 <RNA>
 A:Cross-references: GB:S62043; NID:g385708; PIDN:AA026508.1; PID:g385709
 C:Genetics:
 A:Introns: 238/3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
 F:29-53/Domain: transmembrane #status predicted <TM1>
 F:63-84/Domain: transmembrane #status predicted <TM2>
 F:95-122/Domain: transmembrane #status predicted <TM3>
 F:141-168/Domain: transmembrane #status predicted <TM4>
 F:185-213/Domain: transmembrane #status predicted <TM5>
 F:267-293/Domain: transmembrane #status predicted <TM6>
 F:297-319/Domain: transmembrane #status predicted <TM7>
 F:9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.2%; Score 1678; DB 2; Length 436;
 Best Local Similarity 91.7%; Pred. No. 1.3e-122;
 Matches 322; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 1 WYPEPGPTANSTPAGAGPPAPSGGWAALCVIALTAANSLLIALICTOPALRNT 60
 |||||||
 Db 1 WYPEPGPTANSTPAGAGPPAPSGGWAALCVIALTAANSLLIALICTOPALRNT 60
 QY 61 SNFVLVSFTSDLMVGLVMPAMPALNLYGRWVLAAGLCCLMTAFDVMCCSASILNLCIL 120
 |||||||
 Db 61 SNFVLVSFTSDLMVGLVMPAMPALNLYGRWVLAAGLCCLMTAFDVMCCSASILNLCIL 120
 QY 121 SLDRLILSLPLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTAPAGQC 180
 |||||||
 Db 121 SLDRLILSLPLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTAPAGQC 180
 QY 181 RLASLSPVLVAGSLTFPLPSGAICFTYCRILIAARKQAVQASLTGASQASETLQVP 240
 |||||||
 Db 181 RLASLSPVLVAGSLTFPLPSGAICFTYCRILIAARKQAVQASLTGASQASETLQVP 240
 QY 241 RTRPRGESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 |||||||
 Db 241 RTRPRGESADSRRLATKHSRKALKASLTGILGMEFVTWLPFFVANIQAACDCISPG 300
 QY 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCVHCPEHRPALPPP 351
 |||||||
 Db 301 LFDVLTWLGTCNSTNNPIITPLFMDFKRALGRFLPCVHCPEHRPALPPP 351

RESULT 4

S36794
 beta-1-adrenergic receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
 C:Accession: S36794
 R:Jaeger, J.R.; Link, R.E.; Chruschinski, A.J.; Kobilka, B.K.; Bernstein, D.
 Biochim. Biophys. Acta 1178, 307-309, 1993
 A:Title: Primary structure of the mouse beta(1)-adrenergic receptor gene.
 A:Reference number: S36794; MUID:93372116
 A:Accession: S36794
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-466 <JAS>
 A:Cross-references: EMBL:L10084; NID:g293278; PIDN:AAA02929.1; PID:g293279

C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 25.8%; Score 591.5; DB 2; Length 466;

Best Local Similarity 35.9%; Pred. No. 2.1e-38;
Matches 158; Conservative 63; Mismatches 154; Indels 65; Gaps 17;

```

OY 7 PRANSTPAGAGPPSAPGSGGWAA---ALCVIALTAANSLILALICQPALRTSNP 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 38 PRASLLPPASEG--SAPLSQOWTAGMGLLALLVLLVGNVLAIVAIKTPRLQTLTNL 95
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 64 FLVSLFTSDLMVGLVYMPAMNLALGRVWLAGLCLMTAFDVMCCSAILMLCLISLD 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 96 FIMSLASADLVMLVLPFGATIVVGMWEGSFCELMTSVYLCVTASIEFLCIAID 155
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 124 RYLLISPLRYKLRMTPLRALALVLCAMSLAALASFLPLLGW--HELGHARPPV--PGQ 179
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 156 RYLAITSPPRYOSLTFRARARALVCTVMAISALVSFLPILMHMWRARSDARCYNDPKC 215
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 180 CRLLASLPFLVVASGLTFELPSGALICFTYCRILLARKQAVASLTGMA--QAS 234
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 216 CDFVTRAVAIASSVSVFVPLCIMAFLVLRVREAKQVKKIDSCERRFLSGPRPSP 275
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 235 ETLQVPRTPRGVESADSR-----RLATKHSRKALKAKLTGLIGMFVTLPEFVA 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 276 EFSPPSGPPRPADSLANGSSKRSPRLVALRQKALK---TLGIIMGVFTLCMLPEFLA 332
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 288 NIYQAV--CCICISGFLVDLTWLGYNSTNMPITY---PLEMRDFKRALGRFLPCPR--C 340
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 333 NVYKAFHRDLVPDRLEVFENWLGYSANFNPITYCRSP---DFRKAFORLLCCARRAAC 388
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 341 PREQASLASPSLRTSHSGRPGLS--LQGVLPPLP--PDSSDSDAG----- 385
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 389 RR-----RAAH--GDRPRASGLARAGPPSPGAPSDDDDDAGTTPPARLLEPW 436
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 386 ---SGSSGSLRLTAQLLLPG 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 437 TGCNGSTTVSDSSLDEPG 456
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 5

beta-1-adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Jun-2000

C:Accession: S12591; S40185; A36618

A:Title: Primary structure of the rat beta-1 adrenergic receptor gene.

A:Reference number: S12591; MUID:90356399

A:Accession: S12591

A:Molecule type: DNA

A:Residues: 1-464 <SH1>

A:Cross-References: EMBL:D00634

R:Shimomura, H.; Terada, A.

submitted to the EMBL Data Library, July 1991

A:Reference number: S40185

A:Accession: S40185

A:Molecule type: DNA

A:Residues: 1-25, '26-174, 'R', '175-464 <SH2>

A:Cross-References: EMBL:D00634; NID:g220670; PID:g220671

R:Macchida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Testier, B.; Neve, K.A.; Teal, J.

Biol. Chem. 265, 12960-12965, 1990

A:Title: Molecular cloning and expression of the rat beta-1-adrenergic receptor gene.

A:Accession: A36618

A:Molecule type: DNA

A:Residues: 1-26, '27-160, 'L', '162-174, 'R', '175-264, 'T', '266-464 <MAC>

A:Cross-References: GB:J05561; NID:g203073; PIDN:AAA0792.1; PID:g203074

C:Superfamily: Vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 25.3%; Score 581; DB 2; Length 464;

Best Local Similarity 35.5%; Pred. No. 1.4e-37;
Matches 156; Conservative 63; Mismatches 155; Indels 66; Gaps 17;

```

OY 7 PRANSTPAGAGPPSAPGSGGWAA---ALCVIALTAANSLILALICQPALRTSNP 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 37 PRASLLPPASEG--SAPLSQOWTAGMGLLALLVLLVGNVLAIVAIKTPRLQTLTNL 94
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 64 FLVSLFTSDLMVGLVYMPAMNLALGRVWLAGLCLMTAFDVMCCSAILMLCLISLD 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 95 FIMSLASADLVMLVLPFGATIVVGMWEGSFCELMTSVYLCVTASIEFLCIAID 154
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 124 RYLLISPLRYKLRMTPLRALALVLCAMSLAALASFLPLLGW--HELGHARPPV--PGQ 179
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 155 RYLAITSPPRYOSLTFRARARALVCTVMAISALVSFLPILMHMWRARSDARCYNDPKC 213
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 180 CRLLASLPFLVVASGLTFELPSGALICFTYCRILLARKQAVASLTGMA--QAS 234
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 CDFVTRAVAIASSVSVFVPLCIMAFLVLRVREAKQVKKIDSCERRFLSGPRPSP 273
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 235 ETLQVPRTPRGVESADSR-----RLATKHSRKALKAKLTGLIGMFVTLPEFVA 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 274 APSPPSGPPRPADSLANGSSKRSPRLVALRQKALK---TLGIIMGVFTLCMLPEFLA 330
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 288 NIYQAV--CCICISGFLVDLTWLGYNSTNMPITY---PLEMRDFKRALGRFLPCPR--C 340
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 331 NVYKAFHRDLVPDRLEVFENWLGYSANFNPITYCRSP---DFRKAFORLLCCARRAAC 386
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 341 PREQASLASPSLRTSHSGRPGLS--LQGVLPPLP--PDSSDSDAG----- 385
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 387 RR-----RAAH--GDRPRASGLARAGPPSPGAPSDDDDDAGTTPPARLLEPW 434
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 386 ---SGSSGSLRLTAQLLLPG 402
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 435 AGCNGSTTVSDSSLDEPG 454
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 6

beta 1 adrenergic receptor - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I53053

R:Searles, R.P.; Nipper, V.J.; Machida, C.A.

DNA Seq. 4, 231-241, 1994

A:Title: The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene an

A:Reference number: I53053; MUID:95078456

A:Accession: I53053

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-460 <RES>

A:Cross-References: EMBL:X75540; NID:g510532; PIDN:CAA53226.1; PID:g510533

C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match 24.6%; Score 563.5; DB 2; Length 480;

Best Local Similarity 34.5%; Pred. No. 3.2e-36;
Matches 149; Conservative 62; Mismatches 166; Indels 55; Gaps 14;

```

OY 1 MYPEPPTNSPRAWGAGPPSAPGSGGWAA---ALCVIALTAANSLILALICQPAL 57
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 33 LVP-ASPPASLLPPASEGP--EPLSQOWTAGMGLLALLVLLVGNVLAIVAIKTPRL 89
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 58 RNTSNFVLSFTSDLMVGLVYMPAMNLALGRVWLAGLCLMTAFDVMCCSAILML 117
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 90 QLTFLNFIMSLASADLVMLVLPFGATIVVGMWEGSFCELMTSVYLCVTASIEFL 149
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 118 CLISLDRYLLISPLRYKLRMTPLRALALVLCAMSLAALASFLPLLGW--HELGHARPP 175
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 150 CVIALDRYLAITSPPRYOSLTFRARARALVCTVMAISALVSFLPILMHMWRARSDARCY 209
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

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OY      176 V--PCQCRLLASLPFLVASGLTFPLPSGAICFTYCRIILARQAQAVAS----LTGM 229
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      210 YNDPCCODCVTRAAALASSVSFVPELCLMAFVLVRERQKQVKTKIDSERRFLGSP 269
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      230 ASQASET-----LOVPRTPRGVESADS-----RLATKHRSALKAK 267
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      270 AAPPSPSPSPSPPVAPAPPGRPPRAAAAATAATPALVNGCKRKRRESPTVALRECKALK- 327
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      268 LTLGIILGFEMFTWLPFEFAANIVQAV-CDCISPGLEDVLTEWYGXNSTMPNPIITY---PLF 323
          ||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      328 -TLGIIMGYETLCMLPFELIANVKAFHRELVDRLFVFENNIGLVNSAFNPILTYSRP-- 384
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      324 MDEFRALGRFLPCRPERQASLASPSLRTSMSGPREGISLAQVLPLRP-PDSSDS 382
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      385 --DFRNAFORLICCARAARRHAHGDRPRASCGLARG-----PPSRGAASDDD 435
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      383 DAGSGSSGLRL 394 .
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      436 DDVGATOPARL 447
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT    7
ORRHU1
beta-1-adrenergic receptor - human
C.Species: Homo sapiens (man)
C.Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
C.Accession: A39911
R.Fiettelie, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Koblika, B.K.
Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987
A.Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.
A.Reference number: A39911; MUID:88068509
A.Accession: A39911
A.Molecule type: mRNA
A.Residues: 1-477 <PRI>
A.Cross-references: GB:J03019; NID:g178199; PIDN:AAA5167.1; PID:g178200
C.Genetics:
A.Gene: GDB:ADRB1; ADRB1R
A.Cross-references: GDB:119654; OMIM:109650
A.Map position: 10q25-10q25
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:58-84/Domain: transmembrane #status predicted <TM1>
F:94-121/Domain: transmembrane #status predicted <TM2>
F:133-154/Domain: transmembrane #status predicted <TM3>
F:177-199/Domain: transmembrane #status predicted <TM4>
F:224-245/Domain: transmembrane #status predicted <TM5>
F:325-346/Domain: transmembrane #status predicted <TM6>
F:358-377/Domain: transmembrane #status predicted <TM7>
F:15/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match           24.3% Score 557; DB 1; Length 477;
Best Local Similarity 33.8%; Pred. No. 1e-35;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

OY      1 MYPEGPTANTSPWAGCAPSPAAGSGWVAALCVIALTAANSLLIALLICTOPALRNTP 60
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      33 LVPAASPASLIAPPASESEPQLSQWTAGKMGLMALIVILLVANGNLVIAAIATKPRIQT 92
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      61 SNFFLSLEFSLDMGLVYPAMPNALYGRNYLARGLCLMTAFDVMCCSAISIINLCII 120
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      93 TNLFMSIASADLVGLLVDPGATIYWGRMEXSFCCELMTSDVLCVTASIEITLCVI 152
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      121 SLDRYLTIISPRLRYLRMTPRALALVLGANSIALAFPLPLLGW--HELGHARPV-- 176
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      153 ALDRILAITSPPRIOSLTRARAARGLVCTVWAISALVSFLPLMHMRARESDEARCYND 212
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      177 PGQCRLASLPFLVASGLTFPLPSGAICTFYCRILIARQAQAVAS----LTGMASQ 232
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      213 PRCDCDFVNRAAYIASVSFVPELCLMAFVLYRVFREAQKKVIDSCERRFLGPAPR 272
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      233 ASET-----LOVPRTPRGVESADS-----RLATKHRSALKAKLTITCIL 273
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      273 PPSPPVPAPARPPEGPPRPAAMAAATAPLANGRACKRRPRSLVALLREKALK---TLGI I 329
QY      274 LGMFEVTMLPFFVANIVQAV-CDICSPGLFDYLWLTGICNSTMDPII--PLEMRDFKR 329
       : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      330 MGVFTLCLLPFLANVVAFHRELTPDRLLFVEFFNWLGYAANSFNFIYCRRSP----DFRK 385
QY      330 ALGRPLPCRPCREHQASLASPSLRTHSGRPGLSLOQVLPLPLP-PDSQSDSDASGG 388
       | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db      366 AFQGLLCARRARRARRRHATHGDPRASGCLARPG-----PPSPGAASDDDDDVVGA 438
QY      389 SSGRLT 394
       : : ||
Db      439 TPAPRL 444

RESULT
565459
beta-3-adrenergic receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
C:Accession: S65459; S40504; S31659
R:Pietri-Kouzel, F.; Lemlen, G.; Kapoor, A.; Drumare, M.F.; Archibault, P.; Strosber
Eur. J. Biochem. 230, 350-358, 1995
A>Title: Molecular cloning and pharmacological characterization of the bovine beta3-a
A:Accession: S65459; MUID:95324546
A:Molecule type: mRNA
A:Residues: 1-405 <PIE>
A:Cross-references: EMBL:X85961; NID:g757758; PIDN:CAA59937.1; PID:g757759
A:Experimental source: brown adipose tissue
R:Castella, L.; Muzzin, P.; Revelli, J.P.; Rigquier, D.; Giacobino, J.P.
Biochem. J. 297, 93-97, 1994
A>Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and adenylat
le tat.
A:Reference number: S40503; MUID:94107292
A:Accession: S40504
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 162-298 <CAS>
R:Stoffel, B.; Meyer, H.H.D.
Submitted to the EMBL Data Library, June 1992
A:Description: Bovine beta3-adrenergic receptor, partial genomic sequence.
A:Reference number: S31659
A:Accession: S31659
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 4-5, 'HE', 8-105 <STO>
A:Cross-references: EMBL:x67214
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
F:37-63/Domain: transmembrane #status predicted <TM1>
F:73-101/Domain: transmembrane #status predicted <TM2>
F:113-133/Domain: transmembrane #status predicted <TM3>
F:156-179/Domain: transmembrane #status predicted <TM4>
F:204-225/Domain: transmembrane #status predicted <TM5>
F:293-314/Domain: transmembrane #status predicted <TM6>
F:327-347/Domain: transmembrane #status predicted <TM7>
F:8.26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          24.2%   Score 554; DB 2; Length 405;
Best Local Similarity 33.6%; Pred. No. 1.5e-35;
Matches 143; Conservative 61; Mismatches 156; Indels 66; Gaps 13;

QY      1 MYPERG-TRANSTPWAGMGPPSAPGSGWVAALCVYALTALPAANSLILALICNQPALRN 59
       : : | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db      11 LTPWFDPITLAPNTRNASGLGPVPAVALACALLALVALAVGNGNLVIYAIAIRPRIQT 70
QY      60 TSNEFVLSLFPSDVAWGCVMPAMPMLNALYGRWYLARGICLIIMAPFVMCCSASTLMIC 119
       : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      71 MTNVETSVSLATADLVGLVLYPPGATIALALIGHMPLGVTGCELMISVDVLCYTASTIEFLCA 130
QY      120 ISLDRIYLLIISLPDKRYKRMPLRALALVYGWSLAATASTPLDLIGMHIEIG-----H 171

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F:136,268/Binding site: phosphate (Thr) (covalent) #status predicted
F:259,263/Binding site: phosphate (Ser) (covalent) #status predicted
F:347/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	24.1%;	Score 552.5;	DB 1;	Length 446;
Best Local Similarity	31.2%;	Pred. No. 2.1e-35;		
Matches 143;	Conservative 79;	Mismatches 172;	Indels 65;	Gaps 13;

```

0Y 21 SAPPSSGVW-----AAACVVAITAAANSLLILICITOPALRN-TSNEFVSL 68
Db 7 SAMDGTGLVERDESVRIITACPLISLLITLIGNTLVCAAVIRFRLRSKVTNFEVSL 66
0Y 69 FTSDLMACLVMPRAMLNALLYGRNVTLARGCLILMTAADWCCSILNCLISLDRYLL 128
Db 67 AVSDELVLVAVLMPKAAVEIAGFPFG-SFENINVAEDIMCSTASILNCVISIDRWAI 125
0Y 129 LSPLEKRYLRMTPLRLALAVLCAMSLAALASLURLPILLCMHLEIGHARPPVPG----- 178
126 SSPFEYEKKMTPKAFLILISAMTLVSLISTIPVLSMNR---AKRPSBDGNATSLAET 182
0Y 179 --QCRLLASLDFVLVASGLTFPELPSGALCEFTYCRILLARKQAVQVAST--TTGMAQASE 235
Db 183 IDNCSSLSRTYVAISSVISFYPAIMVITYTRITRAQKQIRIALEBRAVHAKNQ 242
0Y 236 TLQVPRTRPGVESADSRRLTAKSRKALKAKLTGLILGMEFYTWLPFRVANIYQAVCD 295
Db 243 TTTGNGKFEVECSQPSSESSKFFKRETKYLK---TLVSIMGVFCWCMLEPFILNCILPFCG 299
0Y 296 -----CISDGLPVLWILGYCSTNMPIITPLFMDQFKALGRPLPCR-CPRERQA- 346
Db 300 SGEIOPFCIDSTEDYFVFWFGMANSSLNPIIT AFNADFKAFSTLIGCTRICEPATRNAT 358
0Y 347 -----SIASPLRTHSGRPBGSLAQOVLPLPLRPDSDSDSDAGSGGSGSLRLLTAQDLLP 401
Db- 359 ETVSINNNGAMFSSHNHPRGSISKECVLYLIRHAGVSSEDLKKEBAAGIARPLEKSP 418
0Y 402 GEATODPLPLPRAAAAVFNMIDAEPLRP-----HP 434
Db 419 -----ALSVILDTYDVLSLEKIDITONGHR 445

```

RESULT 11
AA1679
beta-3-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999
Accession: AA1679
Muzzlin, P.; Revelli, J.P.; Kuhne, F.; Gocayne, J.D.; McCombie, W.R.; Venter, J.C.; Gitlin
J. Biol. Chem. 266, 24053-24058, 1991
A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down
A:Reference number: AA1679; MUID:92084710
A:Accession: AA1679
A:Molecule type: mRNA
A:Residues: 1-400 <MUD>
A:Cross-references: GB:M74716; NID:9950087; PIDN:AAA74470.1; PID:g202766
A:Experimental source: brown adipose tissue
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
P:8/26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	24.1%;	Score 551.5;	DB 2;	Length 400;
Best Local Similarity	-35.8%;	Pred. NO. 2.3e-35;		
Matches 144;	Conservative 61;	Mismatches 146;	Indels 51;	Gaps 15;

Oy	5	PGPANTSNPA-WGAGP---	PGAPGSGS----	WVAALCVIAL-7AANA	SLIALICQ	54
Db	3	PWPHKNSGLAFMSDAP	PLDPSAANTSGLP	GVMAAALAGLAL	ATVYGNLLVIT	62
Oy	55	PALRNTSNPEFLVLE	FTSDLMYGLVYNNP	PMALNMLXGRVY	LARGLCLLTWTF	114
Db	63	PLQDTTINVEYTS	LATADLVGLLVMP	EGATLTLGMP	IGATGCELTMSV	122

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Oy      115  INLCISIDRLLSPRLSPRYLRLMTPLRALALYVGAASLAALSFLPLGLGMIHLG---- 170
Db      123  ETLCLAVDRYLAVTNPLRGVTLTKRRARAAYLVIMIVATYSFAPIMSGMMHVGADAE 182
Oy      171  ----HARPVGQCRLLASLFPVLVAGSLGFLLFPGALCTTCHILLAARKQAVY---- 222
Db      183  AOECISNRC--CSFASNMRYALLSSVSFYPLLVMLVEYVRAVFVAAKRRFVAREL 239
Oy      223  -----ASLTGGMASOASETLOVPRTPRGVESADSR--RLATFHSKALKAKLTGIL 274
Db      240  GRPEEESPRSPSPSPATVGTPTASDGVPGCGRRPALPLPLGERRALR---TGLIM 295
Oy      275  GMEFYTWLPEFVANIIVQAVC--DCISGLDEVLTWLCYCNSTANPIY---PLFMRDFKR 329
Db      296  GIFSLCWLPFLAVLWLRALVPSLYVPGVFALTALMWLGANSAFPLIYCRSPDFADFR 355
Oy      330  AL----GREFLCPRC---PREROASLASPSLR--TSHSGRP 362
Db      356  LLCSTYGGKGPPEEPKVVTFPPASVASKRONSPLNRDGTGEGERP 397

```

RESULT 12
A53281
beta 3-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A53281; S29808
R:Granneman, J.G.; Lahners, K.N.; Chaudhry, A.
Mol. Pharmacol. 40, 895-899, 1991
A:Title: Molecular cloning and expression of the rat beta 3-adrenergic receptor
A:Reference number: A53281; MUID:92100057
A:Accession: A53281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <GRA>
A:CROSS-references: GB:S73473; NID:g2a1215; PIDN:AAB20702.1; PID:g2a1216
A:Note: Sequence extracted from NCBI backbone (NCBIN:73473, NCBIp:73476)
R:Bensaid, M.; Kaghad, M.; Rodriguez, M.; le Fur, G.; Caput, D.
FEBS Lett. 318, 223-226, 1993
A:Title: The rat beta3-adrenergic receptor gene contains an intron.
A:Reference number: S29808; MUID:93178631
A:Accession: S29808
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-400 <BEN>
A:CROSS-references: GB:S56481; NID:g298306; PIDN:AAB25520.1; PID:g298307
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	24.1%;	Score 551.5;	DB 2;	Length 400;
Best Local Similarity	35.3%;	Pred. No. 2.3e-35;		
Matches 142;	Conservative 61;	Mismatches 148;	Indels 51;	Gaps 15;

```

OY      5  GPGTANSTPA-WGAGP---PSAPGSGS-----WVAALCVIALI-TPAASLILIALCQTO 54
Db      3  PMPHKNGLATWSDAPLIDPDSAAWNTSGLPQVPMMAALAGALLMALATVCGNULVITTHAART 62

OY      55  PALRNTSNFELVSEFTSLDMLAGLVYMPRPMALNALGXWVYLARGLCILLMPFADVMCCSAST 114
Db      63  PRLQTTINVEVTSIATATLAVVLGLVMPRGATLALTGMPGATGCGELMTSDVLCVYAST 122

OY      115  LNLCLISDRRLTLLSPURKYKLRMTPLRALATLVGANSLSAALASFLLGLGMELG---- 170
Db      123  ETLCLADVRDLATLVNPLRYCTVETLKKRRARAAYLVLVIVAEVSPAFIMSOOMRVGDAE 182

OY      171  ----HARPPVGGORLLASLPELVVAGSLFPELPSGAICTCYRILLAAKROVOYASLT 226
Db      183  AOECHSNRC----CSFASNMRYALLSSSVSYETPLVLMLEFVYARVYVAKROR-RLRRE 228

OY      227  TGMASQASSETLOVEPTPP-----GVESADSR--RLATKRSKRALAKLTLGIL 274

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us-09-826-509-449.rpr

[illegible][illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2002, 14:10:35 ; Search time 25.52 Seconds
(without alignments)
2521.937 Million cell updates/sec

Title: US-09-826-509-449

Sequence: 1 MVPEPGPTANSTPAWGAGP.....FNIDPAPELPHPLGIPTN 440

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.potent:*
13: sp.virus:*
14: sp.vertibrate:*
15: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2025	88.4	438	11	063004
2	578	25.2	405	11	09GCR2
3	563.5	24.6	405	6	09GCR56
4	559.5	24.4	405	6	09GCR56
5	558.5	24.4	405	6	09GCR56
6	556	24.3	405	6	09GCR56
7	546.5	23.8	402	5	044198
8	540.5	23.6	407	6	09M200
9	535	23.3	445	13	098841
10	528	23.0	446	13	042315
11	525	22.9	385	5	024038
12	524	22.9	437	13	042316
13	523.5	22.8	391	5	096716
14	511.5	22.3	445	13	098842
15	509.5	22.2	559	11	09GCR71
16	503	21.9	399	5	09N602
17	501	21.9	571	6	09T7M9
18	496	21.6	448	13	098844
19	493.5	21.5	477	5	09BMA9

20	491.5	21.4	380	13	042317	042317 cyprinus ca
21	491	21.4	392	13	09YHA5	09YHA5 myxine glut
22	488.5	21.3	394	5	09NHF3	09NHF3 aplysia cal
23	488	21.3	419	5	077254	077254 boophilus m
24	487.5	21.3	458	13	098843	098843 anguilla an
25	485	21.2	384	13	042318	042318 cyprinus ca
26	483.5	21.1	518	6	09MYT8	09MYT8 oryctolagus
27	483	21.1	515	11	09BML0	09BML0 mus musculu
28	481.5	21.0	508	5	09VCZ3	09VCZ3 drosophila
29	472.5	20.6	470	11	P97842	P97842 rattus norv
30	471.5	20.6	394	5	09NUS6	09NUS6 aplysia kur
31	468	20.4	466	11	09WU25	09WU25 cavia porce
32	464.5	20.3	464	5	09G054	09G054 aedes aegy
33	463	20.2	466	6	09TSM7	09TSM7 sus scrofa
34	462	20.2	359	4	09H199	09H199 homo sapien
35	460.5	20.1	397	11	09D282	09D282 mus musculu
36	458.5	20.0	358	11	09GX37	09GX37 mus musculu
37	458	20.0	429	4	013729	013729 homo sapien
38	458	20.0	499	4	013675	013675 homo sapien
39	457	19.9	466	4	09UD63	09UD63 homo sapien
40	454.5	19.8	408	13	098998	098998 xenopus lae
41	453	19.8	471	11	09QW77	09QW77 cricetus
42	450.5	19.7	377	6	09N263	09N263 sus scrofa
43	450.5	19.7	425	6	09MZU2	09MZU2 oryctolagus
44	450.5	19.7	429	6	09MZU3	09MZU3 oryctolagus
45	450	19.6	455	4	060451	060451 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	438 AA.
063004	063004			
AC	063004			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	5-HT6 SEROTONIN RECEPTOR.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-SPRACUE-DAMELEY, TISSUE-BRAIN STRIATUM;			
RX	MEDLINE=96102917; PubMed=8522986;			
RA	Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Iachowicz J.E.,			
RA	Meltzer H.Y., Sibley D.R., Roth B.L., Hamblin M.W.;			
RT	"Cloning, characterization, and chromosomal localization of a human 5-			
RT	HT6 serotonin receptor."			
RL	J. Neurochem. 66:47-56(1996).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: L41146; AAA92633.1; "			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PRINTS: PR00237; GPCRHOOPS.			
DR	PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.			
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.			
SO	SEQUENCE 438 AA; 46786 MW; DB90403892691A9 CRC64;			

Query Match 88.4%; Score 2025; DB 11; Length 438;
Best Local Similarity 88.9%; Pred. No. 4.3e-136;
Matches 391; Conservative 12; Mismatches 35; Indels 2; Gaps 1;

QY 1 MVPEPGPTANSTPAWGAGPSPAGSGVAAALCVYATLTAANSLLALICITQPAKNT 60
DB 1 MVPEPGPTANSTPAWGAGPSPAGSGVAAALCVYATLTAANSLLALICITQPAKNT 60
QY 61 SNFLVSLFTSIDLAVGLVMPAALNALYGRWVLAELGLMTAFDVMCCSASILNLCI 120

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Db 61 SNFVLSLPSLSDMLVGLVWPPMAMLNLRWMLARGLCLMTLRFDMCCSASTLNCIL 120
OY 121 SLDRLVLLISPLRYKLRMPRLRALALVLAGMSLAALASFLPLLLGHEHCHARRPVYGC 180
Db 121 SLDRLVLLISPLRYKLRMPRLRALALVLAGMSLAALASFLPLLLGHEHCHARRPVYGC 180
OY 181 RLASLPEVYVAGSLFFPLPSGALCFYCYCITLAARKQAVASLTGTGMAQSASELQVP 240
Db 181 RLASLPEVYVAGSLFFPLPSGALCFYCYCITLAARKQAVASLTGTGMAQSASELQVP 240
OY 241 RPRPVEASDRRLATPKHRRKALKKLTGILGFEVWLPPEFVANTQAVQDCISPG 300
Db 241 RPRPVEASDRRLATPKHRRKALKKLTGILGFEVWLPPEFVANTQAVQDCISPG 300
OY 301 LFDVLTLWLGVCNSTMPPIYPLFMRDFKRALGRFLPCPRCPRROASLASPSLRTSHSGP 360
Db 301 LFDVLTLWLGVCNSTMPPIYPLFMRDFKRALGRFLPCVHCPEPRHASPSPMTSHSGA 360
OY 361 RPLGLSLQOVLPLPLPDSOSDSDAGSGSGGLTLTAQLLPGATODDPLPTAAAVNF 420
Db 361 RPLGLSLQOVLPLPLPDSOSDSDAGSGSGGLTLTAQLLPGATODDPLPTAAAVNF 420
OY 421 FNIDPAEPLRPHPLGIPFN 440
Db 419 FVTDVSEPELRPHPLSSPVN 438

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RESULT 2
OQCRR2 PRELIMINARY; PRT: 405 AA.
AC 09CRR2:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).
GN ADRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawaji J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereits P.,
RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AK018378; BAB31185.1; -
DR MGI: 87937; Adrb1
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.

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DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 405 AA; 44741 MW; 4F0F3PBB956E2F4 CRC64;

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Query Match 25.2%; Score 578; DB 11; Length 405;
Best Local Similarity 36.5%; Pred. No. 1.6e-33;
Matches 150; Conservative 61; Mismatches 140; Indels 60; Gaps 15;

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OY 33 LCVIALTAANSLALIALICTOPALRNTSNFVLSFTSDLMGLVWPPMAMLNALXGRW 92
Db 4 LALIVLVGNVNLVLAIAKTRPLDTLNLVLAASADLVGLVFEVGATVWGRW 63
OY 93 VLARGCLMTAFDVMCCSASIIINLCISDRYLILISPLRYKLRMPRLRALALVLAGMS 152
Db 64 EYGSFCELTSTVDLCVNASIEFLCVIALDRYLAITSPPRQSLTLRAARALVCTVNA 123
OY 153 LALASFLPLLLGW--HELCHARRPV--PGCRLASLPEVYVAGSLTFPLPSGALCFY 208
Db 124 ISALVSEFLPLMHMWRASDEARCYNDPKCDFVTRAVAIASVVSFVPLCIMAIFY 183
OY 209 CRILLAARKQAVOVS----LTGMAQSAS-ETLQVPRPVEASDSR-----RLA 256
Db 184 LRVFRERQKQVKKIDSCERFEGPARPPSPPEPGRPADSLANGRSSRRRSRLV 243
OY 257 TKHSRRALKAKLTGILGFEVWLPPEFVANTQAV-CDICISPLFDVLTWLGVCNSTM 315
Db 244 ALREOKALK---TLGILGFEVTLVPLFVLAIVKAFHRLDVLDRPLFVFNWLGYSNAF 300
OY 316 NPITY---PLFMRDFKRALGRFLPCR---CPREKQASLASPLRTSHSGPRLGS--LQ 367
Db 301 NPITYCRSP---DFRKARQLCCARRAACRR-----RAAH-GDRPRASGCLA 344
OY 368 QVPLPLP--PDSOSDSDAG-----SGSSGSLRTAQLLPG 402
Db 345 RAGPPSPGAPSDDDDDAGTTPPARLLEPMWTCNGGTTVDSDSLDEPG 395

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RESULT 3
OQGL56 PRELIMINARY; PRT: 405 AA.
AC 09GL56:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BETA 3 ADRENERGIC RECEPTOR.
GN B3AR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN NCBI_TaxID=9940;
RP SEQUENCE FROM N.A.
RA Forrest R.H., Hickford J.G.H.;
RT Polymorphism within the ovine beta 3 adrenergic receptor gene.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF314203; AAG31166.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 405 AA; 42886 MW; EF4B13BB413EA413 CRC64;

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Query Match 24.8%; Score 563.5; DB 6; Length 405;
Best Local Similarity 34.8%; Pred. No. 1.7e-32;
Matches 146; Conservative 56; Mismatches 163; Indels 55; Gaps 13;

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Db	131	LAVRYLAVTNPRLRGALVTRKRRARAVALIVWVSAVSFAPIKSKMMRWGADAEARCH	190
Qy	172	ARPPPGCRLLASLPFLVVASGLTFELPSSAICFTQCRIILARKANQV-----	222
Db	191	SNPRC---CTFASNNPVALSSVSFTPLVLMLETVARFVAVATROLRLRLRELGRFP	247
Qy	223	-----ASLTGMAQASSETLQVPRTPRGVESADSR--RLATKHSRKALKAKITLIGLG	275
Db	248	EESPAPRSRSGSPGAG-----PYASPVGVPYGRPARLLPLREHRLR---TLGLIMG	299
Qy	276	MEFWTWLDFEFVANIVQAN--CDCISPLGLFDVLTMLGVCNSMNPITY--PLMRQDKRA	330
Db	300	TFLLICWLEFEFVAVNRALGPGSVLSGPTFLALNMLGANSFNPLITICRSP---DERSA	355
Qy	331	LGRELPCEPCREKROASLASPSLRTSHSGPPRGSLTQOVLPLPPDSDSDSDAGSGSS	390
Db	356	FRRLT-C-RCPEEHIAASP-----PRAPSGATVLTSPAGPQPSPLDGCASGCLS	405
RESULT	6		
	09GL57	PRELIMINARY;	PRT; 405 AA.
AC	09GL57;		
DT	01-MAR-2001 (TREMblrel_16, Created)		
DT	01-MAR-2001 (TREMblrel_16, Last sequence update)		
DT	01-JUN-2001 (TREMblrel_17, Last annotation update)		
DE	BETA 3 ADRENERGIC RECEPTOR.		
GN	B3AR.		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Ovis.		
NCBI_TaxID	9940;		
RM	[1]		
RM	SEQUENCE FROM N.A.		
RA	Forrest R.H., Hickford J.G.H.;		
RT	"Polymorphism within the ovine beta 3 adrenergic receptor gene.;"		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	EMBL; AF514200; AAC31163.1; -		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.		
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.		
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.		
NC	SEQUENCE 405 AA; 42928 MW; 6C9FE1EAF90F54B CRC64;		

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Query Match      24.3%; Score 556; DB 6; Length 405;
Best Local Similarity 34.0%; Pred. No. 5, 7e-32;
Matches 146; Conservative 59; Mismatches 151; Indels 74; Gaps

QY      1 MVEPEG-PTANSTPAMGAPESAPBGSGWAAALCVVIALTAANSLILALICTOPALRN 59
Db      11 LTPMPDIPPTLAPNTANASGLPGVPMVAVALGALLALAVLATVGGNLLVIALRTPTLT 70
QY      60 TSNPFLVSLFSDLMGLVYMPRLMALALGRVYLAGLCLLTATAFYVKKCSAILMCL 119
Db      71 MTFNFTVSLADVLAVGLVLPAGATLALTGHPGLVGTGELMTSVYLCVTASITFLCA 130
QY      120 ISLRYYLILSPRLKLTMPRLALALVYLGAMSLAALASFLLLLGHEG-----H 171
Db      131 LAVDRYLAIVNPLRYGALVYTKRRRAAVLVYVYSAVSPAPISKKMRRGADAENORCH 190
QY      172 ARPVPGCCRLLASLPYLVASGLTFEPLPSGALICTFYCRILLAAKQAVY----- 222
Db      191 SNPRC---CFEASNMYPALLSSSYFYLPLVLMFLVAFYAVFVATRLRLRELGRFP 247
QY      223 -----ASLTGMAASQSETLVLPPTPRPGVESADSR--RLATKHSKALKAKLTLGILG 275

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[illegible]

RESULT	7	
ID	004198	PRELIMINARY; PRT; 402 AA.
AC	004198;	
DT	01-JUN-1998 (TREMBLrel. 06, Created)	
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	DOPAMINE RECEPTOR, D1.	
GN	DOP1.	
OS	Apis mellifera (Honeybee).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata	
CC	Apodea; Apidae; Apis.	
OX	NCBI_TaxID=7460;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Baumann A.;	
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.	
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: Y13429; CAA73841.1; -	
DR	InterPro: IPR000276; GPCR_Rhodpsn.	
DR	Pfam: PF00001; 7tm_1; 1.	
DR	PRINTS: PR00237; GPCRHHODPSN.	
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.	
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.	
SO	SEQUENCE 402 AA; 44554 MW; 0B1962DC7F6481DF CRC64;	

[illegible]

QY	378	SDSDS	382
		:	
Db	380	SSADS	384

RESULT 8
Q9M200

ID	Q9M200;	PRELIMINARY:	PRT:	407 AA.
AC	Q9M200;			
DT	01-OCT-2000 (Tremblrel. 15, Created)			
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)			
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)			
DE	BETA-3-ADRENERGIC RECEPTOR.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxId=9823;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RT	Smith T.R., Bidwell C.A., Mills S.E.;			
RL	"Sus scrofa beta3-adrenergic receptor (BAR3) gene.";			
CC	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: AF274407; AAF82301.1; -			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm_1. 1.			
DR	PRINTS: PR00237; GPCRHDOPSN.			
DR	PROSITE: PS00237; G-PROTEIN_REC_F1.1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_REC_F1.2; 1.			
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.			
SQ	SEQUENCE 407 AA; 43610 MW; C6598382A9B38DD9 CXC64;			

Query Match	23.6%	Score 540.5;	DB 6;	Length 407;
Best Local Similarity	33.0%	Pred. No. 7.1e-31;		
Matches 146; Conservative	55;	Mismatches 157;	Indels 85;	Gaps 15

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0Y 5 PGPANSP-----PAGCAGPSPAGCGSWAAALCVIALTAANSLALI 51
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 PMPGNSLSPRPDVSITLAPNNANTSGLPGVPAVALAGALLAPVALATGNNLLVYAI 62
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 52 CTGPALRNTSNFVLEFTSDLMVGLVMPBPAMLNALYGRVTLARGCLMTAFDWCSS 111
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 ARTPRLQMTNWFVTSLATADLVGLLVPRGTTLALGHMPDCAOCELTMSVDVCLVT 122
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 112 ASIATLCLISIDRLLISPLRYLRYLRTPLRALBALVLCANSLAASFLLYLCWHELG- 170
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 ASIETCALADVRLATVNTPLRYALVTKRRARAAYLVWVVAASVAFAPIMSFWMEVGA 182
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 171 -----HARPPVGOCRLASLFPVLVASGLFELPESGALCFYCRILLAAKQ-----A 215
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 DAEQORCHSNPSC---CTFASNMRYALLSSVSFYLELWMLFYANFYVAITSQRLRLR 233
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 220 VQVASLTTGMASSQSETLQVPRPRP-----GYESADSR--RLATKHSRKALAKTLGI 272
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 WELSRPPEESRPAPSSQSPARPMPSPRAGVPSHGCRARRLLRLREHRL--CTGL 296
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 273 LLGMEFYTWLFFFYANVQAVDCISGL-----FDVLTWLGCTNSTMNPITYLEKRD 322
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 297 IMGFETLCWLFEPFVAVNVRAAG--GSLVAVPAFELMLWIGYANSAFNPILTY-CHSPDF 352
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
0Y 328 KRALGRFLPCRCRERQASLASPLRSHSGPRGLSLQOVLRLPLRPDSDSDSDSG 387
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 353 RSAPRRLL-C-RGCPDEHLAASP-----PR-----APSG 386
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Qy	388	GSSGLRTAQDLLGEATQDDPL	410
Db	381	APF-----TLTHPAESRQSPPL	397
RESULT	9		
098841			

ID	098841	PRELIMINARY;	PRT;	445 AA.
AC	098841:			
DT	01-FEB-1997	(TREMblrel. 02,		
DT	01-FEB-1997	(TREMblrel. 02,		
DT	01-JUN-2001	(TREMblrel. 17,		
DE	DOPAMINE D1A1 RECEPTOR.			
NN	D1A1.			

OS *Anguilla anguilla* (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97160583; PubMed=9006917;
RA Cardinaud B., Coudouet S., Vincent J D., Vernier P.;
RT "Early emergence of three dopamine D1 receptor subtypes in
RT vertebrates. Molecular phylogenetic, pharmacological, and functional
RT criteria defining D1A, D1B, and D1C receptors in European eel *Anguilla*
RT *anguilla*.";
RL J. Biol. Chem. 272:2778-2787(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL, U62918; AAC60067.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPSn.
DR PROSITE: PS00237; GPCRHOOPSn.F1.1; 1.
DR PROSITE: PS00263; G-PROTEIN_RECPT.F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SO SEQUENCE 445 AA; 45442 MW; 2A26D945DE39ACDD CRC64;

Query Match	23.3%	Score 535;	DB 13;	Length 445;
Best Local Similarity	35.4%;	Pred. No. 1.9e-30;		
Matches 116;	Conservative 61;	Mismatches 121;	Indels 30;	Gaps 7

Oy	33	LCVVATLAAANSILIALICIGOPALRN-TSFFLVSLTSDSLMGLVWMPAMLNALYGR	91
Dd	28	LSLLLTTLTGNTLCAAVTRRHLRSKVTNFEVVISLAISDLVAIIIVMPKAATEIYGF	87
Oy	92	VWLARGCILLMTAFDVMCCSAIINLCISIDRYLILSPTRYKLIRMTPLPALVLGVAM	151
Dd	88	MPEG-SEFNWVAVDIMKSTSIILNLCTISYDRVIAISSPRYIKRKMTPKAFAFMISYAW	144
Oy	152	SIALASLEPFLILGWHEIGHA-----RPVPQGCRLIASLPVLYASGLTFELPS	201
Dd	147	TLSVLIISTIPQOLNMHKQAAGFPELNTGEREPDPDCSSLRITYAISSSLISPTIV	206
Oy	202	GAICTTYCRILIARKAOVOVASLTGGASOASETLOYRTTPRGVESADSRILATYHSR	266
Dd	207	AIMIYTVRIYRIAOKORIRISALERAESAANKRHSSMGNS----ISESFSSKPFRET	262
Oy	262	KALKAKLLGILLGMFEFTYLPPFPVANIVQAVCD-----CISGLPFDVLTWLGYC	311
Dd	263	KVLK---TLSVIMGVFYOCMLPEFLILCMNVFCEDQAPGAADLPCVASTTFEDVFWVGWA	319
Oy	312	NSTMPIIYPLEMRDFKRALGRPLCPQR	339
Dd	320	NSSLNPILYY-AFNADFERRAKFSTLLGCHR	346

RESULT	10	
042315		
ID	042315	PRELIMINARY; PRT; 446 AA.
AC	042315;	
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	DIA3 DOPAMINE RECEPTOR.	
OS	Cyprinus carpio (Common carp).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi	

RESULT	11
Q24038	
ID	Q24038
AC	Q24038;
DT	01-NOV-1996 (TREMBLrel, 01, Created)
DT	01-NOV-1996 (TREMBLrel, 01, Last sequence update)
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE	DOPAMINE D1-LIKE RECEPTOR (FRAGMENT).
GN	DOPR OR CG9652.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha.
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_Taxid=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RF	STRAIN=CANTON S.
RC	TISSUE=HEAD;
RX	MEDLINE=95237365; Pubmed=7720859;
RA	Sugamori K.S., Demchynshyn L.L., McConkey F., Forte M.A., Niznik H.B., ;
RT	A primordial dopamine D1-like adenylyl cyclase-linked receptor from
RT	<i>Drosophila melanogaster</i> displaying poor affinity for benzazepines." ;
RL	FEBS Lett. 362:131-138(1995).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
OR	EMBL: U22106; AAA85716.1; -.

RESULT	12			
042316				
ID	042316	PRELIMINARY:	PRT:	437 AA.
AC	042316;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
DE	DIA4 DOPAMINE RECEPTOR.			
OS	Cyprius carpio (Common carp).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;			
OC	Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.			
OX	NCBI_TaxId=962;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=RETINA;			
RA	Hirano J., Archer S.N., Djamgoz M.B.A.;			
RL	Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: Y14627; CAAT4971.1; -			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm_1.1.			
DR	PRINTS: PR00237; GPCRHHODPSN.			
DR	PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.			
DR	PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.			
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.			
QO	SOURCE 437 AA; 48707 MW; A4479495F2139CE CRC64;			


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Db 147 TSLSLISFIPVQINMHKQTTSEYDHNGSYGDLILLNDCSSLNRTYAISSSLISFIYIPA 206
QY 203 AICEFTCRILLARKQAVOASITGTMASQASETLOYPRPPREVESADSRRLATKHSRK 262
Db 207 IMVTYTRIYRIKQIRIRSALE--RAESAARNHNSMGNSSSVLESESFKMSFKRETK 264
QY 263 ALKAKTLTGLILGMFTWLPFVAVNVAQVCD-----CTSPGLFDVLTWLYGC 311
Db 265 VLK---TLAVIMGVFCWMLPFILNCMVPECOAHNGSADPFCCVSTTFNVFWFGMA 321
QY 312 NSTMNDIIPLEMRDERKALGRFLPCPR-CPRERQASLASPSLRTSHSGRRPGL 364
Db 322 NSSLNPIIY-AFNADPRKAFSILGCHRLCPGSAITEIVS----INNNGAPQL 370
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QY 336 PCPRCPREQA--SLASP--SL-----RTSHSGPR-----PGLSLQOVLPLP 373
Db 412 RC-QCRRRRRLWLSIRPPLASLDRRRRAFLRPOPSHRSPPGSSPHCTPCGGLGR----- 465
QY 374 LPPDSDSDSAGSG---GSSGLRLTAQLL 400
Db 466 -----HAGDAGFGLOQSKASLRLREWRLL 489
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Search completed: March 15, 2002, 14:14:06
Job time: 211 sec

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RESULT 15
ID 090W71 PRELIMINARY; PRT; 559 AA.
AC 090W71;
BT 01-MAY-2000 (TREMBLrel. 13, Created)
BT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
BT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ALPHA 1-ADRENERGIC RECEPTOR SUBTYPE ALPHA 1D, ALPHA 1D-AR.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92100054; PubMed=1661838;
RA Perez D.M., Plascik M.T., Graham R.M.;
RT "Solution-phase library screening for the identification of rare
RT clones: isolation of an alpha 1d-adrenergic receptor cDNA.";
RL Mol. Pharmacol. 40:876-883(1991).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 559 AA: 59739 MW: 37CD9BD696D3A47D CRC64;
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Query Match 22.2%; Score 509.5; DB 11; Length 559;

Best Local Similarity 33.3%; Pred. No. 1.5e-28;

Matches 150; Conservative 63; Mismatches 158; Indels 79; Gaps 19;

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QY 4 EPGPTA---NSTPAGACPPSPAPG-GSGWVAALCVIALTPAANSLLIAL-ICTQPAL 57
Db 66 EPGAAASGEVNGSAVGLVSNAGVGVEFLAA---FILTRVAGNLVILSVACNRHL 121
QY 58 RNTSNEFLVLTSDLMGLVVMPPAMLNALYGRVVLARGLCILMTAFDVMCCASILNL 117
Db 122 QVTNWFYIVNLAVADLLISAALVPSATMEVGFNAFGRTPCDVMAADVLCCTASILSL 181
QY 118 CLISIDRYILLSPRYKIRMTPLRALALVLGAWSLAALASFLPLLGHWEHGHARPYP 177
Db 182 CTISVDRYVGVHSLKYPAMIERKAAATLALMAVALVSVGP-TLGWKE-----PVP 234
QY 178 GQ---CRLIASLPVLVAGSLTFPLPSGALICTYCRILLARKQAVOASLTGTMASQAS 234
Db 235 PDERFCGITEEYGAIFSSVCSFYLPMAVIYVMYCRVYVARS---TTRSLERAGIKREP 291
QY 235 ETLOY-----PRTPR---PGVESADSRRLATKHSRKAL-----KAKLTGLILGMF 277
Db 292 KASEVVLRIHCGARTSAKAGYPGTQSKGHTLRSSLSVRLKFSREKKAALTAIVGVF 351
QY 278 FVTWLPFEVAVNVAQVCDISP--GLFDVLTWLYGCNSTMNDIIPLEMRDERKALGRFL 335
Db 352 VLKMPPEFFVLPGLSIFPOIKPSGVFVFWLGYFNSCVNDLIYPCSSREKRAFLRL 411
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 14:08:30 ; Search time 14.43 Seconds
(without alignments)
686.171 Million cell updates/sec

Title: US-09-826-509-449
Perfect score: 2292
Sequence: 1 MPEPPTANSTPAMGAGPP.....FNIDPAPELRPHPLGIPTN 440

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/CTOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	24.3	468	2	US-08-390-000A-7
2	557	24.3	477	1	US-08-087-772A-16
3	554	24.2	405	1	US-08-351-473B-2
4	553.5	24.1	365	2	US-08-467-559B-9
5	552.5	24.1	400	1	US-08-351-473B-5
6	552.5	24.1	400	4	US-08-450-962-4
7	552.5	24.1	400	4	US-08-450-962-6
8	552.5	24.1	446	1	US-07-626-618A-21
9	552.5	24.1	446	1	US-08-333-977-21
10	551.5	24.1	400	1	US-07-916-901-6
11	551.5	24.1	400	1	US-07-783-603C-1
12	551.5	24.1	400	1	US-08-351-473B-4
13	551	24.0	477	1	US-08-444-734A-4
14	547.5	23.9	446	2	US-07-969-267B-4
15	546	23.8	388	1	US-08-087-772A-2
16	538.5	23.5	472	1	US-08-194-338-6
17	533.5	23.3	487	1	US-08-444-734A-2
18	533	23.3	408	1	US-08-351-473B-3
19	531	23.2	402	1	US-08-444-734A-6
20	531	23.2	402	1	US-08-087-772A-15
21	531	23.2	408	4	US-07-916-901-2
22	531	23.2	408	4	US-08-450-962-2
23	531	23.2	408	4	US-08-450-962-5
24	524.5	22.9	446	1	US-07-626-618A-22
25	524.5	22.9	446	1	US-08-333-977-22
26	523	22.8	400	2	US-08-103-170-9
27	515.5	22.5	483	1	US-08-194-338-7

28	508	22.2	559	2	US-08-406-855A-20	Sequence 20, Appl
29	508	22.2	559	3	US-09-206-899-20	Sequence 20, Appl
30	503	21.9	572	1	US-08-334-698-2	Sequence 2, Appl
31	503	21.9	572	1	US-08-228-932-2	Sequence 2, Appl
32	503	21.9	572	1	US-08-468-939-2	Sequence 2, Appl
33	503	21.9	572	1	US-08-722-001-30	Sequence 30, Appl
34	503	21.9	572	2	US-08-406-855A-2	Sequence 2, Appl
35	503	21.9	572	2	US-08-722-190-2	Sequence 2, Appl
36	503	21.9	572	3	US-08-244-354-2	Sequence 2, Appl
37	503	21.9	572	3	US-09-206-899-2	Sequence 2, Appl
38	503	21.9	572	5	PCT-US95-04203-2	Sequence 2, Appl
39	499.5	21.8	501	1	US-08-722-001-14	Sequence 14, Appl
40	499.5	21.8	501	2	US-08-467-568-9	Sequence 9, Appl
41	499.5	21.8	501	2	US-09-030-582-9	Sequence 9, Appl
42	499.5	21.8	521	2	US-08-406-855A-19	Sequence 19, Appl
43	499.5	21.8	521	3	US-09-206-899-19	Sequence 19, Appl
44	494.5	21.6	478	3	US-09-292-071-33	Sequence 33, Appl
45	494.5	21.6	478	4	US-09-292-069A-33	Sequence 33, Appl

ALIGNMENTS

```
RESULT 1
US-08-390-000A-7
; Sequence 7, Application US/08390000A
; Patent No. 5985583
; GENERAL INFORMATION:
; APPLICANT: Seallon, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ. ID NO. 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-390-000A-7
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Query Match 24.3%; Score 557; DB 2; Length 468;
Best Local Similarity 33.8%; Pred. No. 96-35;
Matches 144; Conservative 67; Mismatches 169; Indels 46; Gaps 11;

QY 1 MPEPPTANSTPAMGAGPPAPGGSGWAAALCVIALTAANSLLIALICTOPALRMT 60
DB 24 LVPSPPASLIPPPASESPPELQQQWTAGMLMALIVLLVAGNVIVIAIAKTPRLQTL 83

```

QY      61 SNFFVLSFETDLAMGLVMPPAMINALYGRWVLARGICLLMTAFDYMCCSASITLNCI 120
       :|::||::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      84 TNLFTMSIASADLVMLGGLLVVFPGATITYWGKHEIGSFCELMITSVDVLCYTASLETLCVI 143
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 SLDRYLTLSPLRKKRLMRTLPRALALVYGAWSLAALASFPLRLLGW--HELGHARPV- 176
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      144 ALDRLATISPEFRYSOLSTRARRAGILCTVAIAISALVSFLPILMHMMRASDEARECYND 203
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      177 PGCGCLLASLPFVVASGLDFEFLSGAICFYCRHILLARKQAQVNAS-----LTGMASQ 232
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      204 PKCDDFVNRAIVAIASSVSYTYVLCIMAFYYLNVFPEDAOKYAKKIDSCERRFLGGEPARP 253
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      233 ASET-----LOVRRTPRPGEVESADS-----RLATKHSRKALKAKTLTGIL 273
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      264 PSPSPSPVPADAPPGPGRPAPAAATAAPLANGRAGRKRPSLVALRQKMLK---TLGI 320
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      274 LGMFVTNLPFFEVANIQAV-CDCISQLDPVLTWLGYCNSNMNPITY---PLFMRFKR 329
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      321 MGVFLCLLPFLFANVYKAFAFHRELVPDRLLFVFNNWLGVANSAFNPIITCRSP----DFRK 376
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      330 ALGRLLPCRPCPREROASLASFSLRTHSHGPRGLSLQQVLPPLP-PDSDSPSDASG 388
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      377 AFQGLLCARARAARRATHDRRASGCLARPG-----PPSPGASDDDDDDVYGA 429
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      389 SSGRL 394
       :|::|

Db      430 TPAPRL 435

RESULT 2
US-08-087-772A-16
Sequence 16, Application US/0808772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emoring, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
NUMBER OF INVENTIONS: Betas-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 3691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-087-772A-16

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Query Match	24.3%;	Score 557;	DB 1;	Length 477;
Best Local Similarity	-33.8%;	Pred. No. 9.2e-35;		
Matches 144;	Conservative 67;	Mismatches 169;	Indels 46;	Gaps 11;

```

0Y      1 MWPEGGPTANSTPWAGCGPPSAPGSGGWVAALCVVIALFAAANSLLIALLICTOPALARNT 60
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      33 LVPASPSPASLLEPAAESPEPLSQOWTAGMGLMALIIVLLIVAGNVIAIAKTPRLOTJ 92
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      61 SNFPLVSFTSDMLGVMPAMPAMLNALGRWVLARGCLIMTAPFDVMCCSASI LNLCL 120
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      93 TNLFLMTLSADLVNGLLVPGGATIVMGRMFGSFPEELMTSVYLCTYASIE TL CVI 152
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      121 SUDRYLLISPLRYKL RMTPLRALALVLIGAMSIAALASELPULLGN - HELGHARPV-- 176
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      153 ALDRYLATSIPRYSQSLTRARARGIVCTVMAISALVSFLPIILMHMWRAESDARCYN D 212
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      177 PGOCILLASLPVLVASGITFFLPGSAICFYTCRILLAARKOAVQVAS----LTGMASQ 232
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      213 PRCDFVTNRAYAIASVVSFYPLCI MA FYLLRVFEREAKOKKKIDSCERRFLGPARP 272
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      233 ASET-----LQVRTPRPGEVSADS-----RLATKHSRKALKTLTGIL 273
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      273 PSPSPSPVAPARPPGPRPAAAANAATAPLANGRAGRRSRLVALKEQA KAL---TLGI I 329
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      274 LGMEFVTVLPEFVANIVQAV-CDGISPGLFVDVLTWLGYCNSTNPITLY---PLEMRDFKR 329
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      330 MGVFVLCMLPEFLAVVVKAFHRELVPDRLEFEFNWVGANSFNPJIYCSKP----DFRK 385
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      330 ALGRFLPCRCREROASTLASPSLRTSHSGPRGSLQOVLP LPLP-POSDSDPDAGSG 388
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      386 AFQGLLCARRARRRRHAHGDRPRASGLARP G-----PPSPCAASDDDDDDVVYGA 438
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      389 SSGRL 394
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      439 TEPARL 444

RESULT 3
US-08-351-473B-2
Sequence 2, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCIELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-OX PCT

```

RESULT 4
US-08-467-559B-9
Sequence 9, Application US/08467559B
Patent No. 5928690
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: HUMAN AMINE RECEPTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNER, KESSLER, GOLDSTEIN AND FOX, P.L.L.C
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,559B
FILING DATE: 06-JUN-1995

RESULT 5
 US-08-351-473B-5
 : Sequence 5, Application US/08351473B
 : Patent No. 5636440
 : GENERAL INFORMATION:
 : APPLICANT: LENZEN, GERLINDA
 : APPLICANT: KAPOOR, ARCHANA
 : TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
 : TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: OHLON, SPIYAK, MCLELLAND, MAIER & NEUSTADT
 : STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 : CITY: ARLINGTON
 : STATE: VIRGINIA
 : COUNTRY: USA
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-351-473B-5

Query Match 24.1%; Score 552.5; DB 1; Length 400;
Best Local Similarity 35.1%; Pred. No. 1,76-34;
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

Y 5 PGPTANSTPA-WGAP--PSAPGSG-----WVAALCVIAL-TAANSLLIALICTQ 54
D 3 PMPHRNGSLALMSDAPLDPSTAAATSGLPVPMMAALAGALLALATVCGNLVITAIART 62
Y 55 PALNTSFEVLVSLFTSDLMGLVMPAMNALYGRVNLARGICLMTAFDWCCSASI 114
D 63 PRLQTTWFTVSLAALADLVGLVMPGATLALGHWPLDGTGELMTSDVLCVTASI 122
Y 115 LNLCLISDRYLLISPLRYKLRMTPLRALALVLGAMSLALASFLPLLGMHELG---- 170
D 123 ETLCALANDRYLATNPLRYGTIVTKRARAAYLVWYLSAASVAPINSQMWVRGADAE 182
Y 171 ----HARPPVGQCRLLASLPEVLVAGSLTFELPSGAICFTYCRLLLAARKAOVVASLT 226
D 183 AOECHSNPRC---CSFASNMPTAYALLSSVSFYLLPLVWLFYARFVAAKROH-HLRRE 238
Y 227 TGMASQASSETLQVPRTPP-----GVESADSR--RLATKHSRKALAKLTLGLL 274
D 239 LGRFSPEESPSPSPSPATGTPAADGVPCGRPARLLPLREHRAALR---TLGLIM 295
Y 275 GMFEVTLWLPFFVANIIVQAVC--DCISPLFDVLTWLGYNSTNMPIT--PLFMRDCKR 329
D 296 GIFSLCWLPEFLANVLRALAPSLVPSGVFTALNMLGTAANSAPFNVIYICRSPDFDRAFR 355
Y 330 AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP 362
D 356 LLCSYGGRGPEEPRAVTPPASPVEARQSPPLNRFDGYEGARP 397

RESULT 6
US-08-450-962-4
Sequence 4, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROSBURG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: KECK, MAHIN & CATE

STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: FLEIT, Martin; GOLLIN, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-450-962-4

Query Match 24.1%; Score 552.5; DB 4; Length 400;
Best Local Similarity 35.1%; Pred. No. 1,76-34;
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

Y 5 PGPTANSTPA-WGAP--PSAPGSG-----WVAALCVIAL-TAANSLLIALICTQ 54
D 3 PMPHRNGSLALMSDAPLDPSTAAATSGLPVPMMAALAGALLALATVCGNLVITAIART 62
Y 55 PALNTSFEVLVSLFTSDLMGLVMPAMNALYGRVNLARGICLMTAFDWCCSASI 114
D 63 PRLQTTWFTVSLAALADLVGLVMPGATLALGHWPLDGTGELMTSDVLCVTASI 122
Y 115 LNLCLISDRYLLISPLRYKLRMTPLRALALVLGAMSLALASFLPLLGMHELG---- 170
D 123 ETLCALANDRYLATNPLRYGTIVTKRARAAYLVWYLSAASVAPINSQMWVRGADAE 182
Y 171 ----HARPPVGQCRLLASLPEVLVAGSLTFELPSGAICFTYCRLLLAARKAOVVASLT 226
D 183 AOECHSNPRC---CSFASNMPTAYALLSSVSFYLLPLVWLFYARFVAAKROH-HLRRE 238
Y 227 TGMASQASSETLQVPRTPP-----GVESADSR--RLATKHSRKALAKLTLGLL 274
D 239 LGRFSPEESPSPSPSPATGTPAADGVPCGRPARLLPLREHRAALR---TLGLIM 295
Y 275 GMFEVTLWLPFFVANIIVQAVC--DCISPLFDVLTWLGYNSTNMPIT--PLFMRDCKR 329
D 296 GIFSLCWLPEFLANVLRALAPSLVPSGVFTALNMLGTAANSAPFNVIYICRSPDFDRAFR 355
Y 330 AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP 362
D 356 LLCSYGGRGPEEPRAVTPPASPVEARQSPPLNRFDGYEGARP 397

RESULT 7

US-08-450-962-6
: Sequence 6, Application US/08450962
: Patent No. 6274706
: GENERAL INFORMATION:
: APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
: APPLICANT: STROSBURG, Donny
: TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
: TITLE OF INVENTION: GENES
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: KECK, MAHIN & CATE
: STREET: P.O. Box 06110
: CITY: CHICAGO
: STATE: ILLINOIS
: COUNTRY: U.S.A.
: ZIP: 60606-0110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3-1/2" diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450,962
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION NUMBER:
: APPLICATION NUMBER: 08/117,829
: FILING DATE: 08-SEPT-1993
: APPLICATION NUMBER: 07/721,571
: FILING DATE: 25-MAY-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR89/00918
: FILING DATE: 25-JAN-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Fleit, Martin; Gollin, Michael A.
: REGISTRATION NUMBER: 16,900; 31,957
: REFERENCE/DOCKET NUMBER: 47078-042
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 789-3400
: TELEFAX: (202) 789-1158
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 400 residues
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: polypeptide
: DESCRIPTION: polypeptide
: US-08-450-962-6

Query Match 24.1%; Score 552.5; DB 4; Length 400;
Best Local Similarity 35.1%; Pred. No. 1.7e-34;
Matches 141; Conservative 60; Mismatches 150; Indels 51; Gaps 15;

DB 5 PGPRTNSIPA-WGAGP---PSAPGGSG-----WVAALCVVIAL-TAANSLLILICTQ 54
DB 3 PMPHNGSLALMSDAPRTIDPSAANTSGCPGVMAAALAGALLALATVGGNLLVITAIART 62
DB 55 PALRTNSFVLYFTSOLMGLVMPAMALNLYGRVNLVANGICLLMTAFDVMCCSASI 114
DB 63 PRIOTITVNFVTSAAADLVGLVMPGATLALTGHWPLGEGCELMISVDVLCVTASI 122
DB 115 LNLCLISIDRYLLISPLRYKLRMTPLRALALVYLGMSLAALASFLPULLGHEG---- 170
DB 123 ETLCLAVDRYLAIVNPLRYGTLVKRRARAIVLVIVSAVSPAPIMSQWVRGGADE 182
DB 171 ---HARPVPQCRLLASIPFLVAVSGITFLPSGALCTFCRIILAAKQAVVASLT 226
DB 183 AOECHSNRC---CSFASMPYALLSSVSFYLPLVLMFLVYARFVYAKRRR-HLLRE 238
DB 227 TGMASOASETLOWPRTPRP-----GVESADR--RLATKSKRALAKKLTGLTIL 274
DB 239 LGRFSPESPSPSRSPATGTPAPADGVPRCGRRARLLRLREHRLR---TLGLIM 295

DB 275 GMEFVTWLPFVAVNIVQAVC--DCISPLGFDVLTWLGCONSMPLIY---PLFMRDKR 329
DB 296 GIFSLCMLPFLFANVLRALAGPSLVPSGVFLANLWLGANSFNFVYICRSPDFDQARR 355
DB 330 AL---GRFLPCPRC---PREROASLASPSLR--TSHSGPRP 362
DB 356 LLCYSGRGPRPEPRAVTFPASPVEARQSPPLNRFQYEGARP 357

RESULT 8
US-07-626-618A-21
: Sequence 21, Application US/07626618A
: Patent No. 5422265
: GENERAL INFORMATION:
: APPLICANT: Van Tol, Hubert H.M.
: APPLICANT: Civellet, Olivier
: TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allegretti & Witcoff, Ltd.
: STREET: 10 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/626,618A
: FILING DATE: 7 DEC 1990
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5422265nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 90,1092
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: TELEX: 810-221-8317
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 446 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: US-07-626-618A-21

Query Match 24.1%; Score 552.5; DB 1; Length 446;
Best Local Similarity 31.2%; Pred. No. 1.9e-34;
Matches 143; Conservative 79; Mismatches 172; Indels 65; Gaps 13;

DB 21 SAPGGGWV-----AALCVVIALTAANSLLIALICTOPALRN-TSNFFVSL 68
DB 7 SAMDGTGLVERDFESVRIITACFLSLILITLIGMTLVCAAVIRRIULSKVTFEVLISL 66
DB 69 FTSDLWGLVMPAMALNLYGRVNLVANGICLLMTAFDVMCCSASINCLISDRYLI 128
DB 67 AVSDLLVAVLVMPKAVAEIAGFMPRG--SFQINWAFDIMGSTASTILNCLVLSVDRIYAI 125
DB 129 ISPLRYKLRMTPLRALALVYLGMSLAALASFLPULLGHEGHHARPVPVPG----- 178
DB 126 SSPFYERKMRPKAFILISVAMTLSVLSIFPVQLSMHK---AKPTSPSDGNATSLAET 182
DB 179 ---QCRLASLPFLVAVSGITFLPSGALCTFCRIILAAKQAVVASLT-TTGMASQASE 235
DB 183 IDNCDSLSRTYAISSVSIFYIIVAIMVTRYTRIAQKQIRRIALERAHAHVAKNQ 242

Matches	144;	Conservative	61;	Mismatches	146;	Indels	51;	Gaps	15
QY	5	PGPIANSTPA-WGAGP----	PSAPGSGG-----	WVAALCVTAL--TAAANSLLALICTQ	54				
Dd	3	PWPHKNGSLAFWSDAPDTPDSSAANTSGLPVPMWAAALAGALLATVCGNLLVTPAIART	62						
QY	55	PALRNTSNFVLVSEFTSDLMGLVYMPRMLNALYGRVYLAGLCLIKRTAFYVMCCSARI	114						
Dd	63	PRLOQTIVFVFTSYLATADLVGGLVMPGPATLALGHMPLGATGCELMNTSVVPLCVTASI	122						
QY	115	LNLCLISIDRVLLILSPRLRYKRLMPLRLALAYLGMSLALASFLPLILGHELG----	170						
Dd	123	ETLCLADRVRLAYLVNPLRYGTLVYKRRRAAVVLMVIVTSAVSPAPINQWWRGVADAE	182						
QY	171	----HARPPVGQCRLLASLPFLVASGLTFPLPSGAICFTYCRILLARKOAVOY----	222						
Dd	183	AOECHSNRC---CSFASMPRALISSYSFPLPLVLMLETVARFVVAKKORRFRVREL	239						
QY	223	-----ASLTGMAQASQETLQVPTPRPGVESADSR--RLATKHSRKALKAKTLTGILL	274						
Dd	240	GRFPPEESPRSRSPSPATVGT-P-TASDGVSCGRRRARRLLPLGHRKLR---TLGLIM	295						
QY	275	GMFEVTLWLPFVAVANTQAVC--DCISPGLEFDVLTWLGNGYSTMNPILY--P1	329						
Dd	296	GIFSCLWCLPFELVALRLALVGPSELVPSGVFIALNMGVANSFNPILITCRSPDFEADAFRR	355						
QY	330	AL-----GRFLCPRC---PREKQASLASSLR--TSHSGPRP	362						

RESULT 12
US-08-351-473B-4
Sequence 4, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

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;      LENGTH: 400 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-351-473B-4

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Query Match	24.1%;	Score 551.5;	DB 1;	Length 400;
Best Local Similarity	35.1%;	Pred. No. 2e-34;		
Matches 141;	Conservative 62;	Mismatches 148;	Indels 51;	Gaps 15;

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OY      5  PGPANSPPA-WGAGP---PAPGSGS-----WVAALCVIAL-TPAANSILIALCTQ  54
Db      3  PMPHKNGLAMWSAPPLIDPSAANTSGLPGVMAAALAGALLALATYGGMLVITTAIRT  62
OY      55  PALRNTSNFLLVSLTSDLMVGLVYMPMAMINALYGRWVLARGCLLTMTAFDYWCSCASI  114
Db      63  PRLQITVFWFVSTLATADVLVGLLMPBPATLITTHMPILGATCEJMTSVDLVCVTASI  122
OY      115  LNLCLISIDRLVLLLSPLRYLRLTPPLRALALVIGANSIALASFLPILLGWHELG----  170
Db      123  ETLCALAVDRILAVTNPLRGVLTLYKRRARAAYVLVWIVASIVSFAPIMQMRVGDAD  182
OY      171  ----HARPPVPGOGRLLASLPELVYASGLPEELPESGAICFTYCRILLAKOAVNASLT  226
Db      183  AOECHSNRC--CSFASNMPIALLSSSVSYLEPLVLMFLVYAVAFVAVAKRÖR-RLIRE  238
OY      227  TGMASOASETLQVPRTPP-----GESADSR-RFLATKHSRKALKAKTILGILL  274
Db      239  LGRPPEESPRSPSPSPATVGTPTASDVGPSCGRPRAPLLPGEHRLR---TTLGIM  295
OY      275  GMFEVYTWLPFFVANIIVQAVC--DCISQLEDVLTWLGICYSINMPITY---PLEMRDKR  329
Db      296  GIFSCWLPPEFLAVYIRALVSPSLVPSGVTALNMLCYANSAENPLIYCRSPDFDRAFR  355
OY      330  AL----GRFLCPRC---PRRROSLASPSLUR--TSHSGRP  362
Db      336  LLCSTGGGPEEPKRVYTFPASPVASRONSPLNRFDGEGEP  397

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RESULT 13
US-08-444-734A-4
Sequence 4, Application US/08444734A
Patent No. 5610282
GENERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monσμα, Frederick J.
APPLICANT: Mahan, Lawrence C.
APPLICANT: Mcvittle, Loris D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
receptor linked to adenylyl cyclase activation and
expression of the receptor protein in plasmid-transfected
cell lines
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,734A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA: US 08/029,917
APPLICATION NUMBER:

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1      BILLING DATE: 03-MAR-1993
2
3      PRIOR APPLICATION DATA:
4
5      APPLICATION NUMBER: US 07/548,714
6
7      FILING DATE: 06-JUL-1990
8
9      ATTORNEY/AGENT INFORMATION:
10
11      NAME: Altman, Daniel E.
12
13      REGISTRATION NUMBER: 34,115
14
15      REFERENCE/DOCKET NUMBER: NIH065.001FW
16
17      TELECOMMUNICATION INFORMATION:
18
19      TELEPHONE: (714) 760-0404
20
21      TELEFAX: (714) 760-9502
22
23      INFORMATION FOR SEQ ID NO: 4:
24
25      SEQUENCE CHARACTERISTICS:
26
27      LENGTH: 477 amino acids
28
29      TYPE: amino acid
30
31      STRANDEDNESS: single
32
33      TOPOLOGY: linear
34
35      MOLECULE TYPE: protein
36
37      HYPOTHETICAL: NO
38
39      ANTI-SENSE: NO
40
41      FRAGMENT TYPE: internal
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Query Match	24.0%;	Score 551;	DB 1;	Length 477;
Best Local Similarity	33.8%;	Pred. No. 2.6e-34;		
Matches 144;	Conservative 66;	Mismatches 170;	Indels 46;	Gaps 11

Qy	1	WVEELGEPANSTI	RAMGAGPSPAFEGSGVAAADCV	LAATLAAMASSTL	LAALCTOPALRNT	80	
Dp	33	LVPASPPASL	PPASESEPEPL	SQOMTAGMGLMAL	IELLIVAGNV	LVIVAAKPRLOTL 92	
Qy	61	SNPFVLVS	FTDMLVGLV	VMPRAALN	MLNGLRWVL	ARGCLCTIMTAFVDMGCSASTNLCL 120	
Dp	93	TNLEIMSLAS	ADLMVGL	LVVEFGAT	IYVWGMEYGS	FFCECLIMTSVDVL	CVYATASETLCLVI 132
Qy	121	SUDRYLL	LSPLRYK	LRMTPLRAL	ALVGLGMS	LAALASFLPLRLGWN	-HEIGNARPPV-- 176
Dp	153	ALDRYLAT	TSPEFRYQ	SLTLTRARAG	VLCTWVAIS	ALVSPILPLIMHMWRAS	DEARRCYND 212
Qy	177	PGOCRLAS	LEFVLV	ASGLTF	FLFDPG	AICFTYGC	ILILAAKROVQVAS----LTTGASQ 232
Dp	213	PKCDEFTV	NRAVYA	LAASSVSP	FYVLC	IMAFYLV	FEFEADQOYKMKIDSCERRFLGPARP 272
Qy	233	ASET	-----	LQYPR	PRPVEG	ASD-----	RLATKHSKRLKAKTLTGLT 273
Dp	273	PSPSPPV	PAPAPAP	PPGPP	AAAAAT	APLANG	RAGKRRPSTVALRBOKALK---TLGIT 329
Qy	274	LGMFEFTWL	LPFVANI	VOAV-CDC	ISPGLE	FVNLTWL	GYCSTNMPRIIY---PLFMRDFKR 339
Dp	330	MGVETL	ICMLPFL	LANVYKA	IFREL	VPRLP	FFFMWLTGYANSAPRIIYCNSP----DFRK 385
Qy	330	ALGRPL	PCPRC	PRRQAS	SLASPS	RTSHSG	PRGLSLQOVLPLPLP--PDSUDSDSDAGSGG 388
Dp	386	AFQGL	LCCARRA	ARRRHATH	GDPRAS	GCLARP	-----PPSPGAAASDDDDDDVVGA 438
Qy	389	SSGLRL	394				
Dp	439	TPPARL	444				

RESULT 14
 US-07-969-267B-4
 Sequence 4, Application US/07969267B
 Patent No. 5862835
 GENERAL INFORMATION:
 APPLICANT: Weinstein, Richard L.
 APPLICANT: Hartig, Paul R.
 TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
 TITLE OF INVENTION: Receptor And Uses Thereof
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP

```

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,267B
FILING DATE: 05-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/551,448
FILING DATE: 10-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: D1
US-07-969-267B-4

Query Match
Best Local Similarity 30.9%; Score 547.5; DB 2; Length 446;
Matches 142; Conservative 80; Mismatches 172; Indels 65; Gaps 13;

21 SAPGGSGWV-----AAALCVIALTAANSLIALICTOPALRN-TSNEFLVSL 68
7 SAMDTGLVERDFSVRLITACFLSLILLSTLGLTGLVCAAVIRFRLRSKYTNFVLSL 66
69 FTSDLAMGLVWPPAMLANLYGRWYLARGLCLMTAFDVMCCSASLNLCLSLDRYLLI 128
67 AVSDLLVALVWPKRAVEIAGFMFG-SECNIMWAFDMICSTASILDLCVIVDRYMAI 125
129 LSPRLRYKLMPTLRALAVLIGAMSLAALASFLPLLGWHELGHARPPVG----- 178
126 SSPRYEKRMTPKAFILISVAMTSLVLSIFIPVQLSMHK---AKPTSDGNGATSLAET 182
179 --QCRLASLPFLVYASGTFEFLPSGAICFTYCRILLAAKQAVOYASL--TTGMAQASE 235
183 IDNCSSSLSRFYAISSVSYFYPVAIMIVTYTRYIRIAOKOIRRIALERAARVAKNQ 242
236 TLQVTRTPGVESADSRRLATKHSRKALKAKLTGLIIGMFVWLPFEVANIYQAVOD 295
243 TTGNGKPEGCSQPPSSRFMSFKRETQYK--TLVIMGVVCCMLPFLINCLIPFGC 299
296 -----CISPLGLFVLITWLGYNSTMPNIYPLFMDFKRALGRFLPCPR-CPRERQA- 346
300 SGEOTPCFIDSTFDFVFWFGWANSINPIY-AFNADRKAFSTLLGCRYLCPATNNMI 358
347 -----SLASPLSRITSHSGRRPLSLQOVLPLPDPDSDSDAGSGGSGGLRLTAQLLP 401
359 ETVSINNGAAMFSSHHEKRGISKECNLYVLIPIHAVGSSSEDLKKKEAGIARPLEKISP 418
402 GEATQDPLPTRAAAVNFENIDPAEELRP-----HP 434
419 -----ALSVILDYDTVDSELEKIOTITONGQHP 445

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RESULT 15
US-08-087-772A-2
Sequence 2, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmlas, Clara
APPLICANT: Emorine, Jean L.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-087-772A-2

Query Match
Best Local Similarity 23.8%; Score 546; DB 1; Length 388;
Matches 139; Conservative 59; Mismatches 137; Indels 52; Gaps 16;

5 PGPTANSRPA-MGAGP---PSAPGSGG-----WAAALCVIAL--TAANSLIALICTQ 54
3 PMPHRGSLALMSDAPTLDPSSAANTSGLPVPMALAGALLALAVGCLLVITAIART 62
55 PALRNTSNFVLSFTSDMLVGLVWPPAMLANLYGRWYLARGLCLMTAFDVMCCSASI 114
63 PRIQTTNVEFVSLAADDLVGGLVMPGATLALTGHPGLGETGCEIANTSVDLCTASI 122
115 LNCICISLDRYLLISPLRYKLMPTLRALAVLIGAMSLAALASFLPLLGWHELG----- 170
123 ETLCALAVDRIYALVNPRLRYGLVTKRRARAAYLVMIYSAVSPFAPINSHQNRVGADE 182
171 ----HARPPVQOCRLASLPFLVYASGTFEFLPSGAICFTYCRILLAAKQAVOYASLT 226
183 ADECHSNPRC---CSFASMPYALLSSVSFTPLVLVLFYVARVAVAKRQ-RHLRRE 238
227 TGMASOASTLQVPTPRP-----GVESADR--RLATKHSRKALKAKLTIGILL 274
239 LGRFSPESPPSPSRSPATGTPAAPDGVPPCGRRPARLLPLREHRLR---TLGLIM 295
275 GMEFVTLWLPFEVANIYQAVC--DCISPLGLFVLITWLGYNSTMPNIY---PLFMDFKR 329
296 GLFSLCWLPEFLANVRLALAGPSLVPSGVFIALNWLGTANSAPNVIYCRSP---DFRD 351
330 ALGRFLPCP---RCPRERQASL--ASP 351

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Db 352 AFRRL-CSYGGGPEPPRAVTFPASP 377

Search completed: March 15, 2002, 14:10:25
Job time: 115 sec
